

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_r2p model

Run on: May 28, 2005, 15:38:35 ; Search time 90 Seconds
(without alignments)
5586.539 Million cell updates/sec

Title: US-09-869-566-4
Perfect score: 1134
Sequence: 1 taactcacatgctcgcact.....cgactctagagatcccgcg 650

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 segs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seg length: 0
Maximum DB seg length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame_r2p.model -DEV=tlp
-O=/cgn2_1/USPTO.spool_p/US09869566/runat_27052005_163130_19900/app_query.faeta_1.839
-DB=A.Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09869566 @CGN_1_1_154 @runat_27052005_163130_19900 -NCPU=6 -ICPU=3
-NO_WMAP -LANG=QUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -IONGLOO
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A.Geneseq_16Dec04:
1: geneseqp19808:
2: geneseqp19908:
3: geneseqp20008:
4: geneseqp20018:
5: geneseqp20028:
6: geneseqp20038:
7: geneseqp20038:
8: geneseqp20048:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1059	93.4	203	3	AA96933 Human IL-
2	906	79.9	192	3	AA95297 Human int
3	906	79.9	192	8	ADN05880 Antisort
4	902	79.5	197	3	AA95300 Human int
5	895	78.9	198	4	AA885138 Interleuk
6	895	78.9	207	3	AA96938 Human IL-
7	895	78.9	218	3	AA970927 Human z11
8	895	78.9	218	3	AA91885 Primate i1
9	895	78.9	218	3	AA95299 Human int
10	895	78.9	218	3	AA96940 Human IL-

11	895	78.9	218	3	AA828266 Human int
12	895	78.9	218	4	AA847186 IL-1 re1a
13	895	78.9	218	4	AA668116 Human int
14	895	78.9	218	4	AA885136 Interleuk
15	895	78.9	218	8	AD788306 Human int
16	895	78.9	218	8	AD115868 Human int
17	895	78.9	218	8	ADN05012 Antisort
18	895	78.9	218	8	ADN05012 Antisort
19	895	78.9	218	8	ADN05012 Antisort
20	895	78.9	218	8	ADN05012 Antisort
21	895	78.9	218	8	ADN05012 Antisort
22	895	78.9	218	8	ADN05012 Antisort
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24	895	78.9	218	8	ADN05012 Antisort
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26	895	78.9	218	8	ADN05012 Antisort
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37	895	78.9	218	8	ADN05012 Antisort
38	895	78.9	218	8	ADN05012 Antisort
39	895	78.9	218	8	ADN05012 Antisort
40	895	78.9	218	8	ADN05012 Antisort
41	895	78.9	218	8	ADN05012 Antisort
42	895	78.9	218	8	ADN05012 Antisort
43	895	78.9	218	8	ADN05012 Antisort
44	895	78.9	218	8	ADN05012 Antisort
45	895	78.9	218	8	ADN05012 Antisort

ALIGNMENTS

RESULT 1	AA96933 standard; protein; 203 AA.
ID	AA96933 standard; protein; 203 AA.
AC	AA96933;
XX	
XX	31-OCT-2000 (first entry)
XX	
DE	Human IL-1RA fused to heterologous signal sequence.
XX	
KW	hIL-1RA; human interleukin-1 receptor antagonist-1; IL-1IP; osteopathic;
KW	interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW	anti-arthritis; antitubercular; respiratory; anti-ischemic; vaccine;
KW	dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX	
OS	Homo sapiens.
XX	
EH	Key
FT	Peptide
FT	Peptide
FT	Peptide
FT	Peptide
FT	Peptide
FT	Protein
PN	WO200039297-A2.
XX	
PD	06-JUL-2000.
XX	
PF	22-DEC-1999;
XX	
PR	23-DEC-1998; 98US-0113430P.

PR 22-JAN-1999; 99US-0116843P.
 PR 13-APR-1999; 99US-0129122P.
 PA (GENH) GENENTECH INC.
 XX
 XX
 PI Goddard A, Pan J;
 XX
 DR WPI; 2000-452395/39.
 DR N-PSDB; AAA51592.
 XX
 PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
 preventing and treating e.g. inflammation, asthma and psoriasis.
 XX
 PS Claim 22; Fig 2; 143pp; English.
 XX
 CC An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-1 β) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (IL-1Ra1) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-1 β polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patient's production of the polypeptide or to rectify
 CC mutations that lead to the production of an active peptide). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-1 β protein expression and activity which may be used to
 CC treat disorders associated with inappropriate IL-1 β expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease
 CC
 SO Sequence 203 AA;
 Alignment Scores:
 Pred. No.: 1,76e-112 Length: 203
 Score: 1059.00 Matches: 203
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 93.39% Indels: 0
 DB: Gaps: 0
 US-09-869-566-4 (1-650) x AAY96933 (1-203)
 QY 10 ATGTCTGCACTTGTGATCTTGTGAGCTGAGCTGATGATCAAGACGAT 69
 DB 1 MetSerAlaLeuLeuLeuAlaValGlyAlaAlaValAlaAspTyrLysAspAsp 20
 QY 70 GACGACAGCTTGCGCGCGGAATTCAGCTCTTGGAGAGTCCAAAGGTGAAGAACTTA 129
 DB 21 AspAspLysLeuAlaAlaAlaAlaSerAlaLeuCyArgGlyProLysValLysAlaLeu 40
 QY 130 AACCCGAGAAATTCAGCATTCATGACCAAGATCACAAGTACTGCTTCGACTTGAG 189
 DB 41 AsnProLysLysPheSerIleHisAspGlnAspHisLysValLeuValLeuAspSerGly 60
 QY 190 AATCTATGACGATTCAGATTAATAAATCATATACGCCGACAGATCTTCTTGGATTAGCC 249
 DB 61 AsnLeuIleAlaValAlaProAspLysAsnTyrIleArgProLysIlePhePheAlaLeuAla 80
 QY 250 TCATCTTGAGCTGAGCTCTGCGGAGAAAGAACGATTCCTCGGGGGTCTCTAA 309
 DB 81 SerSerLeuSerSerAlaSerAlaGluLysGlySerProLysLeuLeuGlyValSerLys 100
 QY 310 GGGGAGCTTTGTCTTACTGTGACCAAGATTAAGACCAAGTCAATCCCTTCAGCTG 369
 DB 101 GlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSerHisProSerLeuGlnLeu 120
 QY 370 AAGAGGAGAAATGATGAAGCTGGCTGCCAAAGAAAGATCAGACGCCGGCTTCATC 429
 DB 121 LysLysGluLysLeuMetLysLeuAlaAlaGlnLysGluSerAlaArgArgProPheIle 140

QY 430 TTTTATAGGGCTCAGGTGGGCTCTCTGGAACATGCTGGAGTGGCGGCTTCACCCGGATGG 489
 DB 141 PheTyrArgAlaGlnValGlySerTyrAsnMetLeuGluSerAlaAlaHisProGlyTyr 160
 QY 490 TTCATCTGACCTCTCGCAATTGTATAGAGCTGTGGGGTGAAGATTAATTGGAAC 549
 DB 161 PheIleCysThrSerCysAsnCysAsnGluProValGlyValThrAspLysPheGluAsn 180
 QY 550 AGGAAACATGTAATTTTCATTTCAACACGATTTGCAAGTGAATGAGCCCAAGTGG 609
 DB 181 ArgLysHisIleGluPheSerPheGlnProValCysLysAlaGluMetSerProSerGlu 200
 QY 610 GTCAGCGAT 618
 DB 201 ValSerAsp 203
 RESULT 2
 ID AAY95297
 AA AAY95297 standard; protein; 192 AA.
 XX
 AC AAY95297;
 DT 12-SEP-2000 (first entry)
 XX
 DE Human interleukin-1 zeta.
 XX
 XX Interleukin-1 zeta; IL-1 zeta; human; therapy; inflammation; fever.
 XX
 OS Homo sapiens.
 XX
 PN WO200036108-A2.
 PD 22-JUN-2000.
 XX
 PF 14-DEC-1999; 99WO-US029549.
 PR 14-DEC-1998; 98US-0112163P.
 PR 10-NOV-1999; 99US-0164675P.
 XX
 PA (IMWV) IMMUNEX CORP.
 XX
 PI Sims JE, Smith DE, Born TL;
 XX
 DR WPI; 2000-442387/38.
 DR N-PSDB; AAA27918.
 PT Isolated interleukin-1 (IL-1) zeta nucleic acid and splice variants
 PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
 PT identifying genes associated with diseases such as gliucoma, and insulin-
 PT dependent diabetes mellitus.
 PS Claim 10; Page 8; 87pp; English.
 XX
 CC The present sequence is that of human interleukin-1 zeta (IL-1 zeta), a
 CC member of the IL-1 family. The sequence was determined by translation of
 CC the nucleotide sequence of isolated IL-1 zeta cDNA (see AAA27918). IL-1
 CC zeta mRNA is generated from exons 3-6 of the IL-1 zeta locus. The mRNA is
 CC expressed most strongly in the testis, prostate, colon, brain, placenta, the
 CC lung, foetal liver and lymph node stroma, lung, testis and placenta. The
 CC invention is directed to novel, purified and isolated IL-1 zeta, IL-1
 CC zeta splice variants and Xrec2 polypeptides (see AAY95297-301), the
 CC nucleic acids (see AAA27918-22) encoding such polypeptides, processes for
 CC production of recombinant forms of such polypeptides, and their uses. The
 CC polypeptides can be used to study cellular processes such as immune
 CC regulation, cell proliferation, cell death, cell migration, cell-to-cell
 CC interaction and inflammatory responses, to identify proteins associated
 CC with IL-1 zeta, to screen for potential inhibitors, and to prepare
 CC antibodies. In particular, they can be used to activate and/or inhibit
 CC the activation of vascular endothelial cells and lymphocytes, induce
 CC and/or inhibit the induction of local tissue destruction and fever,
 CC inhibit and/or stimulate macrophages and vascular endothelial cells to
 CC produce IL-6, induce and/or inhibit the induction of prostaglandins,

CC nitric oxide synthetase, and metalloproteinases, and upregulate and/or
 CC inhibit the upregulation of molecules on the surface of vascular
 CC endothelial cells

XX Sequence 192 AA:

Alignment Scores:

Pred. No.:	7e-95	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	3	Gaps:	0

US-09-869-566-4 (1-650) x AAY95297 (1-192)

```

QY 106 AAGAGTCCAAAGTGAAGAACTTAAACCGAAGAAATTGACATTGATGACGATGAC 165
DB 22 ArgGlyProIyValIysAsnLeuAnProIyLysPheSerIleHisPrgInAspHis 41
QY 166 AAGATGATGCTGCTGAGCTCTGGGATCTCATGAGCTCCAGATTAATAAATGATACG 225
DB 42 LysValLeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrlIleArg 61
QY 226 CCAGAGATCTTCTTTCATTAAGCTCATCTGAGCTGAGCTGCGGAGAAAGAGAT 285
DB 62 ProGluIlePhePheIleuAlaSerSerIleSerIleSerIleGluIySer 81
QY 286 CCGATTCTCTGGGGGTCTCTTAAAGGAGTTTGTCTTACTGTGACAAAGATAAGAA 345
DB 82 ProIleLeuLeuGlyValSerIySgIyGluPheCyLeuTyrcyAspLysAspLysGly 101
QY 346 CAAAGTCATCCATCCCTTCAGCTGAGAGAAAGAACTGATGAGCTGCTGCCAAAG 405
DB 102 GlnSerHisProSerLeuGlnLeuIySbGlyLysLeuMetLysLeuAlaGlnLys 121
QY 406 GAATGACAGCGCGGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 465
DB 122 GlnSerAlaArgArgProPheIlePheTyArgAlaGlnValGlySerTrpAsnMetLeu 141
QY 466 GAGTGGCGGCTTCACCCCGAGATGCTTCATCTGACCTCTGCAATTGATGAGCTGTT 525
DB 142 GlnSerAlaAlaHisProGlyTrpPheIleCyThrSerCysAsnCyAsnGlnProVal 161
QY 526 GGGGTGACAGTAATAATTGAGAAACAGAAACATTTGATTTGATTAACCAAGTTTGC 585
DB 162 GlyValThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProVal 181
QY 586 AAGCTGAATGAGCCCGAGTGAAGTCAAGCAT 618
DB 182 LysAlaGlnMetSerProSerGlnValSerAsp 192

```

RESULT 3

ADN05880 standard; protein; 192 AA.

ADN05880;

01-JUL-2004 (first entry)

Antipsoriatic protein sequence #1103.

antipsoriatic; gene therapy; psoriasis; diagnosis.

Homo sapiens.

WO2004028479-A2.

08-APR-2004.

25-SEP-2003; 2003MO-US030907.

25-SEP-2002; 2002US-0414006P.

XX (GENT) GENENTECH INC.

PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;

PI Wu ID;

DR MPI; 2004-305105/28.

DR N-PSDB; ADN05879.

PT New PRO nucleic acid or polypeptide, useful for preparing a

PT pharmaceutical composition for diagnosing or treating psoriasis in a

PT mammal.

PS Claim 9; SEQ ID NO 2275; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for

XX treating psoriasis or a sequence having at least 80% identity to the

XX above sequences. The nucleic acid is useful for preparing a composition

XX for diagnosing or treating psoriasis in a mammal. This sequence

XX corresponds to one of the polypeptides of the invention.

XX Sequence 192 AA:

US-09-869-566-4 (1-650) x ADN05880 (1-192)

Alignment Scores:

Pred. No.:	7e-95	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	8	Gaps:	0

```

QY 106 AAGAGTCCAAAGTGAAGAACTTAAACCGAAGAAATTGACATTGATGACGATGAC 165
DB 22 ArgGlyProIyValIysAsnLeuAnProIyLysPheSerIleHisPrgInAspHis 41
QY 166 AAGATGATGCTGCTGAGCTCTGGGATCTCATGAGCTCCAGATTAATAAATGATACG 225
DB 42 LysValLeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrlIleArg 61
QY 226 CCAGAGATCTTCTTTCATTAAGCTCATCTGAGCTGAGCTGCGGAGAAAGAGAT 285
DB 62 ProGluIlePhePheIleuAlaSerSerIleSerIleSerIleGluIySer 81
QY 286 CCGATTCTCTGGGGGTCTCTTAAAGGAGTTTGTCTTACTGTGACAAAGATAAGAA 345
DB 82 ProIleLeuLeuGlyValSerIySgIyGluPheCyLeuTyrcyAspLysAspLysGly 101
QY 346 CAAAGTCATCCATCCCTTCAGCTGAGAGAAAGAACTGATGAGCTGCTGCCAAAG 405
DB 102 GlnSerHisProSerLeuGlnLeuIySbGlyLysLeuMetLysLeuAlaGlnLys 121
QY 406 GAATGACAGCGCGGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 465
DB 122 GlnSerAlaArgArgProPheIlePheTyArgAlaGlnValGlySerTrpAsnMetLeu 141
QY 466 GAGTGGCGGCTTCACCCCGAGATGCTTCATCTGACCTCTGCAATTGATGAGCTGTT 525
DB 142 GlnSerAlaAlaHisProGlyTrpPheIleCyThrSerCysAsnCyAsnGlnProVal 161
QY 526 GGGGTGACAGTAATAATTGAGAAACAGAAACATTTGATTTGATTAACCAAGTTTGC 585
DB 162 GlyValThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProVal 181
QY 586 AAGCTGAATGAGCCCGAGTGAAGTCAAGCAT 618
DB 182 LysAlaGlnMetSerProSerGlnValSerAsp 192

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RESULT 4

AA95300 standard; protein; 197 AA.

AA95300

CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
CC modulators are useful for treating chronic and acute inflammation.
CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
CC psoriasis and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
CC polynucleotides are useful as diagnostic reagents and for chromosome
CC identification. The present sequence represents the IL-1H4 mature
CC polypeptide

SQ Sequence 198 AA;

Alignment Scores:

Pred. No.:	1.3e-93	Length:	198
Score:	895.00	Matches:	169
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	4	Gaps:	0

US-09-869-566-4 (1-650) x AAB85138 (1-198)

QY 112 CCAAGGTGAGAACTTAAACCGAAGAAATTGAGATTCAGACGAGATCAAAAGTA 171
DB 30 ProlysvallvshnleuhsnProlyslvshpserillehshspglshpslshvsl 49
QY 172 CTGGTCTTGAGCTCTGGGAATCTCATAGAGATTCCAGATAAAACTACATACGCCAGAG 231
DB 50 LeuValLeuAspserGlyasnleuilealValProAspIysasnIylleArgProGlu 69
QY 232 ATCTTTCTTGATTCATCCCTCATCTTGGAGCTCAGCTTCGCGAAGAAAGAGATCCGATT 291
DB 70 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluysGlySerProIle 89
QY 292 CTCCTGGGGGCTCTTAAAGGGAGATTGCTCTACTGATGCAAGATTAAGGCAAAAGT 351
DB 90 LeuLeuGlyValSerIlyserIyGlnPheCysLeuIlyCysAspIysAspIysGlyGlnSer 109
QY 352 CATCCATCCCTTCAGCTGAGAGAGAGAACTGATGAGCTGGCTGCCAAAAGGATCA 411
DB 110 HisProSerLeuGlnleuIlysluIyblenMeIyLeuAlaIaGlnIyGlnIySer 129
QY 412 GCAAGCGGGCCCTTCACTCTTTTAAAGGCTCAGGTGGGCTCCTGGAACATGCTGAGTGG 471
DB 130 AlaArgArgProPheIlePheIlyArgAlaGlnValIlySerIlyPasnMeIyGlnIySer 149
QY 472 GCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGGCTGTGGGGTG 531
DB 150 AlaAlaIleAspProGlyIlyPheIleCysIlyIlySerCysAsnIyAsnIyProValIlyVal 169
QY 532 ACAGATTAATTTGAGAACAGAAACATTTGATTTTCAACAGATTTTCAAGCT 591
DB 170 ThrAspIyPheGlnAsnArgIyshIstIeGlnPheSerPheGlnProValCysIyAla 189
QY 592 GAAATGAGCCCAAGTGAAGTCAAGCAT 618
DB 190 GluMetSerProSerGluValSerAsp 198

RESULT 6

ID AAY96938 standard; protein, 207 AA.

AAY96938;

31-OCT-2000 (first entry)

Human IL-1 receptor antagonist 1 long.

hIL-1RAIL; human interleukin-1 receptor antagonist-1 long; IL-1lp;

osteopathic; interleukin-1-like polypeptide; anti-inflammatory;

KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KW gene therapy.

OS Homo sapiens.

PN WO200039297-A2.

PD 06-JUL-2000.

PF 22-DEC-1999; 99WO-US030720.

PR 23-DEC-1998; 98US-0113430P.

PR 22-JAN-1999; 99US-0116843P.

PR 13-APR-1999; 99US-0129122P.

PA (GETH) GENENTECH INC.

PI Goddard A, Pan J;

DR WPI; 2000-452395/39.

DR N-PSDB; AAY51601.

PS Claim 22; Fig 15; 143bp; English.

CC An isolated nucleic acid molecule encoding an interleukin-1-like

CC polypeptide (IL-1lp) that retains one or more activities of the peptide

CC from which it is derived, such as the IL-18R binding activity of a human

CC interleukin-1 receptor antagonist-1 (hIL-1RAI) polypeptide, is new. The

CC nucleic acids may be used in molecular engineering applications, e.g.

CC hybridization assays and chromosome and gene mapping studies, for

CC recombinantly producing the IL-1lp polypeptide or for producing gene

CC knock out animals to study the role of the protein in metabolism and

CC disease processes (conversely, gene therapy protocols may be used to

CC supplement a patient's production of the polypeptide or to rectify

CC mutations that lead to the production of in active peptides). The

CC peptides produced may be used to screen for and produce modulators (e.g.

CC antibodies) of IL-1lp protein expression and activity which may be used to

CC treat disorders associated with inappropriate IL-1lp expression and

CC activity, such as inflammatory disorders, asthma, arthritis,

CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress

CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,

CC psoriasis, graft versus host disease and/or inflammatory bowel disease

CC

SQ Sequence 207 AA;

Alignment Scores:

Pred. No.:	1.32e-93	Length:	207
Score:	895.00	Matches:	169
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	3	Gaps:	0

US-09-869-566-4 (1-650) x AAY96938 (1-207)

QY 112 CCAAGGTGAGAACTTAAACCGAAGAAATTGAGATTCAGACGAGATCAAAAGTA 171
DB 39 ProlysvallvshnleuhsnProlyslvshpserillehshspglshpslshvsl 58
QY 172 CTGGTCTTGAGCTCTGGGAATCTCATAGAGATTCCAGATAAAACTACATACGCCAGAG 231
DB 59 LeuValLeuAspserGlyasnleuilealValProAspIysasnIylleArgProGlu 78
QY 232 ATCTTTCTTGATTCATCCCTCATCTTGGAGCTCAGCTTCGCGAAGAAAGATCCGATT 291
DB 79 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluIyGlySerProIle 98
QY 292 CTCCTGGGGGCTCTTAAAGGGAGATTGCTCTACTGATGCAAGATTAAGGCAAAAGT 351

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Db      99 LeuLeuGLyValSerLySGlyGluPheCySLeuTyrcYsaSPlysaSPlySGlyGlnSer 118
QY      352 CATTCATCCCTCAGCTGAAGAAGGAAACTGATGAGCTGGCTGCCCAAGAAAGATCA 411
Db      119 HisProSerLeuGlnLeuLySGlyGlnLysLeuLysLeuLysLeuLysLeuLysLeuLys 138
QY      412 GCACGCCGCCCTTCATCTTTATATAGGGCTCAGAGTGGGCTCCTGGAACATGCTGAGTGG 471
Db      139 AlaArgArgProPheIlePheTyArgAlaGlnValGlySerTrpPheMetLeuGlnSer 158
QY      472 GGGGCTCACCCCGGATGTTTCATCTGACCTCTCTGAATTTATATAGGCTGTGGGGTG 531
Db      159 AlaAlaHisProGlyTrpPheIleCysTrpSerCysAsnCysAsnGlnProValGlyVal 178
QY      532 ACAGATAAATTTGAGAAGCAGAAACATTTGATTTTCATTTCAACCCAGTTTGCAAGCT 591
Db      179 TrpAspLysPheGlnLysAsnArgLysHisIleGluPheSerPheGlnProValCysLysAla 198
QY      592 GAAATGAGCCCCAGTGAGTCAAGCAT 618
Db      199 GluMetSerProSerGlnValSerAsp 207

RESULT 7
AAY70927
ID      AAY70927 standard; protein; 218 AA.
XX
AC      AAY70927;
XX
DT      05-SEP-2000 (first entry)
XX
DE      Human zll1a4 protein.
XX
KM      Human interleukin-1; IL-1; zll1a4 protein; inflammation; arthritis;
KW      psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW      anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW      chronic neuropathology; respiratory disease syndrome; restenosis;
KW      acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;
KW      anti-arthritis; anti-psoriasis; antibacterial; immunosuppressive;
KW      anti-anaemic; neuroprotective; vasotropic;
KW      anti-human immunodeficiency virus; HIV.
XX
OS      Homo sapiens.
XX
FH      Key
FH      Domain
FT      Location/Qualifiers
FT      /label= Beta_strand
FT      60..64
FT      /label= Beta_strand
FT      65..67
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      68..72
FT      /label= Beta_strand
FT      73..76
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      77..79
FT      /label= Beta_strand
FT      80..89
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      90..96
FT      /label= Beta_strand
FT      97..107
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      108..113
FT      /label= Beta_strand
FT      114..117
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      118..123
FT      /label= Beta_strand
FT      124..131
FT      /note= "Variable loop region involved in receptor

```

```

FT      binding"
FT      132..138
FT      /label= Beta_strand
FT      139..153
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      154..160
FT      /label= Beta_strand
FT      161..164
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      165..169
FT      /label= Beta_strand
FT      170..174
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      175..179
FT      /label= Beta_strand
FT      180..186
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      187..189
FT      /label= Beta_strand
FT      190..200
FT      /note= "Variable loop region involved in receptor
FT      binding"
FT      201..204
FT      /label= Beta_strand

Domain
WO200024899-A2.
XX
PD      04-MAY-2000.
XX
PF      27-OCT-1999; 99WO-US025038.
XX
PR      27-OCT-1998; 98US-00179614.
XX
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PI      West RR, Sheppard PO, Gao Z;
XX
DR      WPI, 2000-350740/30.
DR      N-PSDB; AAD00210.
XX
PT      Immunomodulatory interleukin-1 homolog zll1a4 proteins, useful for
PT      treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT      disease, leukemia.
XX
PS      Claim 4; Fig 2; 88pp; English.
XX
CC      The present sequence is the human interleukin (IL)-1 homolog zll1a4
CC      protein. This protein contains a core structure of 12 beta-strands wound
CC      into a beta-barrel, with the beta-strands separated from each other by
CC      loops. The loops between these beta-strands are highly variable among the
CC      family members and are believed to be involved in receptor binding. The
CC      zll1a4 proteins modulate inflammation and other immunological processes
CC      and are therefore useful for treatment of arthritis, psoriasis, septic
CC      shock, graft-versus-host disease and leukaemia. Other diseases that may
CC      be modulated by zll1a4 proteins include cancer, anaemia, inflammatory
CC      bowel disease, acute and chronic neuropathologies, shock, respiratory
CC      disease syndrome, restenosis and acquired immune deficiency syndrome
XX
SQ      Sequence 218 AA;
XX
Alignment Scores:
Pred. No.: 1.34e-93 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: 3 Gaps: 0
US-09-869-566-4 (1-650) x AAY70927 (1-218)

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QY 112 CCAAGGTGAAGACTTTAAACCCGAAGAAATTCAGATTTCATGACCGAGATCAAAAGTA 171
Db 50 ProlyValValysAsnLeuAsnProlySlyPheSerIleHisAspGlnAspHislyVal 69
QY 172 CTGGTCTTGAGACTCTGGGAATCTCATAGCAGTTCCAGATTAATAACATACGCCAGAG 231
Db 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspIlyAsnIlyrIleArgProGlu 89
QY 232 ATCTTTCTTGATTAAGCTTCATCTTGAAGTCAAGCTCTTCGCGAAGAAAGAAATCCGATT 291
Db 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleAlaGlnlySglYserProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGGTAAGACAAAGT 351
Db 110 LeuLeuGlyValSerlySglYglnPheCySleuIlyrCyAspIlyAspIlySglYlnSer 129
QY 352 CATCCATCCCTTCAGCTGGAAGAGAACTGATGAAGCTGAGCTGCCCAAGAAATCA 411
Db 130 HisProSerLeuGlnLeuIlySlySglYlyLeuMetIlyLeuAlaGlnlySglYlnSer 149
QY 412 GCACGCCGGGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGAGTGG 471
Db 150 AlaArgArgProPheIlePheIlyrArgAlaGlnValGlySerTriPAsnMetLeuGlnSer 169
QY 472 GGGGCTCACCCCGGAGTTCATCTGCACTCTGCAATTGATATAGAGCTGTGGGGTG 531
Db 170 AlaAlaHisProGlyTrpPheIleCySlnSerCyAsnIlyAsnGlnProValGlyVal 189
QY 532 ACAGATAATTTGAGAACAGAAACATTTGATTTTCAACGAGTTTCAAGCT 591
Db 190 ThrAspIlyPheGlnAsnIlySlyHisIleGlnPheSerPheGlnProValCySlySAla 209
QY 592 GAAATGAGCCCCAGTAGAGTCAAGCT 618
Db 210 GluMetSerProSerGlyValSerAsp 218

RESULT 8
ID AAY91885 standard; protein; 218 AA.
XX
XX AAY91885;
XX
XX 19-JUL-2000 (first entry)
XX
XX Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
XX
XX Primate interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
XX hypoglycemia; plasma iron; plasma zinc; acute liver response;
XX plasma copper.
XX
XX Mammalia.
XX
XX Key Location/Qualifiers
XX FH 58..64 /label= beta_strand_1
XX FT 69..74 /label= beta_strand_2
XX FT 75..80 /label= beta_strand_3
XX FT 91..96 /label= beta_strand_4
XX FT 100..106 /label= beta_strand_5
XX FT 107..113 /note= "forms a loop which is part of a primary binding
XX segment to the IL-1 receptor type"
XX FT 118..126 /label= beta_strand_6
XX FT 131..136 /label= beta_strand_7
XX FT 154..161 /label= beta_strand_8
XX FT

```

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FT Domain 163..169
FT FT /label= beta_strand_9
FT Domain 176..180
FT FT /label= beta_strand_10
FT Domain 185..204
FT FT /label= beta_strand_11
FT Domain 201..204
FT FT /label= beta_strand_12
XX
XX MO200017363-A2.
XX
XX 30-MAR-2000.
XX
XX 17-SEP-1999; 99WC-US020868.
XX
XX 18-SEP-1998; 98US-00156966.
XX
XX (SCHER) SCHERING CORP.
XX
XX Timans JC;
XX
XX MPI, 2000-283588/24.
XX
XX N-PSDB; AAA08513.
XX
XX New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
XX for diagnostic and therapeutic purposes, comprises a 128 amino acid
XX sequence.
XX
XX Claim 1; Page 103-104; 110pp; English.
XX
XX PS
XX
XX The present sequence is an alternative primate interleukin-1 like
XX molecule, designated IL-1-zeta. The 12 beta strands, indicated in the
XX features table, fold into a beta-trefoil fold. The specification claims
XX an isolated or recombinant polypeptide that: (a) specifically binds
XX polyclonal antibodies generated against at least a 12 consecutive amino
XX acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see
XX AAY91885); and (b) comprises at least one sequence selected from:
XX AAY91886-903 or AAY91904-06. The preferred 12 consecutive amino acid
XX segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to
XX play a role in systemic inflammatory reactions, such as fever,
XX hypoglycemia, reduced plasma iron and zinc, the acute response of the
XX liver, and increase plasma copper. IL-1-zeta binding compounds
XX (comprising antigen binding sites) and IL-1-zeta polypeptides are also
XX useful for both diagnostic and therapeutic purposes
XX
XX SQ Sequence 218 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1,34e-93 Length: 218
XX Score: 895.00 Matches: 169
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 78.92% Indels: 0
XX DB: 3 Gaps: 0
XX
XX US-09-869-566-4 (1-650) x AAY91885 (1-218)
QY 112 CCAAGGTGAAGACTTTAAACCCGAAGAAATTCAGATTTCATGACCGAGATCAAAAGTA 171
Db 50 ProlyValValysAsnLeuAsnProlySlyPheSerIleHisAspGlnAspHislyVal 69
QY 172 CTGGTCTTGAGACTCTGGGAATCTCATAGCAGTTCCAGATTAATAACATACGCCAGAG 231
Db 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspIlyAsnIlyrIleArgProGlu 89
QY 232 ATCTTTCTTGATTAAGCTTCATCTTGAAGTCAAGCTCTTCGCGAAGAAAGAAATCCGATT 291
Db 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleAlaGlnlySglYserProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGGTAAGACAAAGT 351
Db 110 LeuLeuGlyValSerlySglYglnPheCySleuIlyrCyAspIlyAspIlySglYlnSer 129

```

QY 352 CATCATCCCTTCAGTGAAGAGAGAACTGATGAGCTGCTGCCCAAGAAAGATCA 411
Cc 130 HisProSerLeuIndLeuIysLysGIuLysLLeuMetLysLeuAlaIaGlnLysGIuSer 149
QY 412 GCACGCGCGCGCTTCATCTTTTATAGGGCTCAGGTGGCTCCCGGAACATGCTGAGTG 471
Cc 150 AlaArgArgProHeIlePheIyrArgAlaGlnValGIuSerTrpAsnMetLeuGIuSer 169
QY 472 GCGGCTCACCCCGAGATGTTTCATCTGCACCTCCTGCATTTGTAATGAGCTGTGGGGTG 531
Cc 170 AlaAlaHisProGIuTrpPheIleCysTrnSerCysAsnCysAsnGIuProValGIuVal 189
QY 532 ACAGATTAATTTGAGAACACAGAAACATTTGATTTTCATTACCACTGGTCAAGCT 591
Cc 190 ThrAspLysPheGIuAsnArgLysHisIleGIuPheSerPheGIuProValCysLysAla 209
QY 592 GAAATGAGCCCGCTGATGCTCAGCGAT 618
Cc 210 GIuMetSerProSerGIuValSerAsp 218
Db

RESULT 9

AA95299
ID AAY95299 standard; protein; 218 AA.

AC AAY95299;
DT 12-SEP-2000 (first entry)
XX

DE Human interleukin-1 zeta splice variant TDZ.1.

XX Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1;
KW testis-derived zeta variant; therapy; inflammation; fever.

OS Homo sapiens.

XX MO200036108-A2.

XX 22-JUN-2000.

PF 14-DEC-1999; 99MO-US029549.

PR 14-DEC-1998; 98US-0112163P.

PR 10-NOV-1999; 99US-0164675P.

XX (IMMV) IMMUNEX CORP.

PI Sims JE, Smith DE, Born TL;

XX MPI; 2000-442387/38.

DR N-PSDB; AAA27920.

PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and insulin-
PT dependent diabetes mellitus.

PS Claim 10; Page 11; 87pp; English.

XX The present sequence is that of splice variant TDZ.1 (testis-derived zeta
Cc variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated
Cc from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and the encoded
Cc protein is probably a functional IL-1 like molecule. TDZ.1 mRNA is
Cc expressed most strongly in the kidney, skeletal muscle, testis, prostate,
Cc ovary, colon, small intestine, liver, placenta, lung, tonsil, foetal
Cc liver, lymph node and bone marrow. The invention is directed to novel,
Cc purified and isolated IL-1 zeta, its splice variants and Xrec2
Cc polypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22)
Cc encoding such polypeptides, processes for production of recombinant forms
Cc of such polypeptides, and their uses. The polypeptides can be used to
Cc study cellular processes such as immune regulation, cell proliferation,
Cc cell death, cell migration, cell-to-cell interaction and inflammatory
Cc responses, to identify proteins associated with IL-1 zeta, to screen for
Cc potential inhibitors, and to prepare antibodies. In particular, they can

Cc be used to activate and/or inhibit the activation of vascular endothelial
Cc cells and lymphocytes, induce and/or inhibit the induction of local
Cc tissue destruction and fever, inhibit and/or stimulate macrophages and
Cc vascular endothelial cells to produce IL-6, induce and/or inhibit the
Cc induction of prostaglandins, nitric oxide synthetase, and
Cc metalloproteases, and upregulate and/or inhibit the upregulation of
Cc molecules on the surface of vascular endothelial cells
Cc

SQ Sequence 218 AA;

Alignment Scores:

Pred. No.: 1,34e-93 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: Gaps: 3

US-09-869-566-4 (1-650) x AAY95299 (1-218)

QY 112 CCAAGGTGAAGAACTTAACCCGAAAGAAATTGACATTCATGACCAGGATCAAAAGTA 171

Db 50 ProLysValLysAsnLeuAsnProLysLysPheSerIleHisAspGlnAspHisLysVal 69

QY 172 CTGTCTCTGAGCTCTGGGAATCTCATTCAGATGTTCCAGATTAATACTTACATACCCAGAG 231

Db 70 LeuValLysAspSerGIuAsnLeuIleAlaValProAspLysAsnTrpIleArgProGIu 89

QY 233 ATCTTCTTGATTTAGCCCTTCATCCCTTGAGCTCAGCTCTCGCGAAGAAAGAGTCCGAT 291

Db 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGIuSerProIle 109

QY 292 CTCCTGGGGGTCTTAAAGGGGAGTTTGTCTCTACTGTCAGCAAGATTAAGCAAAAGT 351

Db 110 LeuLeuGIuValSerLysGIuLysLeuTrpCysAspLysAspLysGIuSer 129

QY 352 CATCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGCTGCCCAAGAAAGATCA 411

Db 130 HisProSerLeuGIuIndLysGIuLysLeuMetLysLeuAlaAlaGlnLysGIuSer 149

QY 412 GCACGCGCGCGCTTCATCTTTATAGGCTCAGGTGGGCTCCTGGAAACATGCTGAGTCG 471

Db 150 AlaArgArgProPheIlePheTrpArgAlaGlnValGIuSerTrpAsnMetLeuGIuSer 169

QY 472 GCGGCTCACCCCGAGATGTTTCATCTGCACCTCCTCAATTGTAATGAGCTGTGGGGTG 531

Db 170 AlaAlaHisProGIuTrpPheIleCysTrnSerCysAsnCysAsnGIuProValGIuVal 189

QY 532 ACAGATTAATTTGAGAACACAGAAACATTTGATTTTCATTCAACAGTTGCAAGCT 591

Db 190 ThrAspLysPheGIuAsnArgLysHisIleGIuPheSerPheGIuProValCysLysAla 209

QY 592 GAAATGAGCCCGCTGATGCTCAGCGAT 618

Db 210 GIuMetSerProSerGIuValSerAsp 218

RESULT 10

AA956940
ID AAY96940 standard; protein; 218 AA.

AC AAY96940;

DT 31-OCT-2000 (first entry)

XX Human IL-1 receptor antagonist 1 V.

XX hIL-1RA1V; human interleukin-1 receptor antagonist-1; IL-1IP;

XX osteopathic; interleukin-1-like polypeptide; anti-inflammatory;

XX anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;

XX anti-ischemic; dermatological; immunomodulatory; gastrointestinal;

OS Homo sapiens.

XX MO200039297-A2.
 PN
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-US030720.
 XX
 PR 23-DEC-1998; 98US-0113430P.
 PR 22-JAN-1999; 99US-0116843P.
 PR 13-APR-1999; 99US-0129122P.
 XX
 PA (GETH) GENENTECH INC.
 PI
 PI Goddard A, Pan J;
 XX
 XX WPI; 2000-452395/39.
 DR
 DR N-PSDB; AAA51604.
 XX
 PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
 PT preventing and treating e.g. inflammation, asthma and psoriasis.
 XX
 PS Claim 22; Fig 19; 143pp; English.
 XX
 XX An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-11p) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (IL-1Ra) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-11p polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patients production of the polypeptide or to rectify
 CC mutations that lead to the production of in active peptides). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-11p protein expression and activity which may be used to
 CC treat disorders associated with inappropriate IL-11p expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease
 XX
 XX Sequence 218 AA;
 SQ
 Alignment Scores:
 Pred. No.: 1.34e-93 Length: 218
 Score: 895.00 Matches: 169
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.92% Indels: 0
 DB: 3 Gaps: 0
 US-09-869-566-4 (1-650) x AAY96940 (1-218)
 QY 112 CCAAGGTGAGAACTTAAACCCGAGAATTGAGATTCATGACGAGATCAGAAAGTA 171
 DB 50 ProlyValValahenunehunProlySlySpheSerIleHisepolmshpsllySval 69
 QY 172 CTGGTCTTGAGACTCTGGGAAATCTCATGAGAGTTCCAGATAAAACTACATACGCCGAG 231
 DB 70 LeuValIleuAspserCylsenuleuIleAlaValProAspIlyssnrylIleArgProGlu 89
 QY 232 ATCTTTTGGCATTTAGCCATCTATCTTGAGCTCAGCTTCGGGAGAAAGGAATCCGATT 291
 DB 90 IlePhePheAlaIleuAlaSerSerIleuSerSerAlaSerAlaGluIlySGlySerProIle 109
 QY 292 CTCCTGGGGGCTCTCTAAAGGGAGATTTTGTCTCTACTGTCGACAAAGGATAAGCAAGT 351
 DB 110 LeuIleuGlyValSerIlySGlyIlyPheCysIleuTyCysAspIlyAspIlySGlyIlySer 129
 QY 352 CATTCATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTGGCTCCCAAAAGGATCA 411
 DB 130 HisProSerIleuGlnIleuIlySlySGlyIlySleuMetIlyleuAlaIleuGlnIlySGlyIlySer 149

QY 412 GCAGCCGGCCCTTCATCTTTTATAGGGCTCAGTGAGGCTCCTGGAAACATGCTGAGTGC 471
 DB 150 AlaArgArgProPheIlePheTyArgAlaGlnValGlySerTrpAsnMetIleuGlnSer 169
 QY 472 GCGGCTCACCCCGAGATGTTTCATCTGCACCTCTGCAATTTGATAGAGCTTGAGGAGTG 531
 DB 170 AlaAlaIleProGlyTrpPheIleCysIleuSerCysAsnCyAsnGlnuProValGlyVal 189
 QY 532 ACAGATTAATTTGAGAACAGGAAACACATTTGATTTTTCATTCACACGATTTGGCAAGCT 591
 DB 190 ThrAspIlyPheGluAsnArgIlyshIleGluPheSerPheGlnuProValCysIlySala 209
 QY 592 GAAATGAGCCCGCAGTGAGGTCAGCGAT 618
 DB 210 GluMetSerProSerGlnuValSerAsp 218
 RESULT 11
 AAB28266
 ID AAB28266 standard; protein; 218 AA.
 XX
 AC AAB28266;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE Human interleukin-1 homologue IL-1H4.
 XX
 KW Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;
 KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
 KW transplant rejection; graft versus host disease; infection; stroke;
 KW ischemia; acute respiratory disease; allergy; asthma; restenosis;
 KW brain injury; AIDS; bone disease; osteoporosis; cancer;
 KW congestive heart failure; atherosclerosis; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200063226-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 14-APR-2000; 2000WO-US010207.
 XX
 PR 16-APR-1999; 99US-00293625.
 XX
 PA (SMK) SMITHKLINE BEECHAM CORP.
 XX
 PI Young PR, McDonnell PJ;
 XX
 DR WPI; 2000-687155/67.
 DR N-PSDB; AAC66727.
 XX
 PT Interleukin-1 homolog useful for treating conditions such as chronic and
 PT acute inflammation, septicemia, autoimmune diseases ischemia, acute
 PT respiratory disease, allergies, and asthma.
 XX
 PS Claim 1; Page 28-29; 30pp; English.
 XX
 CC The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 is
 CC useful for treating conditions such as chronic and acute inflammation,
 CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,
 CC psoriasis, and arthritis), transplant rejection, graft versus host
 CC disease, infection, stroke, ischemia, acute respiratory disease,
 CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.
 CC osteoporosis), cancer, congestive heart failure, atherosclerosis, and
 CC Alzheimer's disease, related to either an excess of, or an under-
 CC expression of, IL-1H4 polypeptide activity
 XX
 SQ Sequence 218 AA;
 Alignment Scores:
 Pred. No.: 1.34e-93 Length: 218
 Score: 895.00 Matches: 169
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.92% Gaps: 0
 DB: 3 Indels: 0

US-09-869-566-4 (1-650) x AAB28266 (1-218)

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QY 112 CCNAAAGTGAAGAACTTAAACCCGAAAGAAATTGAGATTTCATGACCGAGATCACAAGTA 171
DB 50 ProlysVallyAsnLeuAsnProlyslsPheSerIleHisaspGlnsphislyVal 69
QY 172 CTGGCTCTGAGCTCTGGAGATCTCATAGCAGATTCCAGATAAACAATACATAGCCGAGAG 231
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProaspLysAsnTyrIleArgProGlu 89
QY 232 ATCTCTTTGATTAAGCTCATCTTGAAGTCAAGCTGAGCTGCGGAAAGAAAGTCCGATT 291
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnlysglySerProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTCGACAGATTAAGACAAAGT 351
DB 110 LeuLeuGlyValSerlysglyGlnPheCysLeuTyrCysAspLysAspLysGlyInsSer 129
QY 352 CATCCATCCCTTCAGCTGAGAAAGAGAAAGAACTGATGAGCTGGCTGCCAAAGAAATGA 411
DB 130 HisProSerLeuGlnLeuLysGlnLysLeuMetLysLeuAlaAlaGlnLysGlyInsSer 149
QY 412 GCACGCCGGCCCTTCATCTTTTATAGAGGCTCAGGTGGGCTCTGGAACAATGCTGAGTGC 471
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrAsnMetLeuGlnSer 169
QY 472 GCGGCTCACCCCGATGGTTTCATCTGCACTCTGCAATTGATAGAGCTGTGGGGTG 531
DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnProValGlyVal 189
QY 532 ACAGATAAATTTGAGAACAAGAAACATGATTTTTCATTTCACAGATTGGCAAGT 591
DB 190 ThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProValCysLysAla 209
QY 592 GAAATGAGCCCGCATGAGTCAAGCGAT 618
DB 210 GluMetSerProSerGlnValSerAsp 218

RESULT 12
AAB47186
ID AAB47186 standard; protein; 218 AA.
XX AAB47186;
AC
XX
DT 29-JUN-2001 (first entry)
XX
DE IL-1 related polypeptide.
XX
KW Interleukin-1-related polypeptide; HRP-MLT cell; T-cell; inhibition;
XX natural killer activity; immune system; gene therapy; immunodeficiency.
XX
OS Homo sapiens.
XX
PN EP1092773-A2.
XX
PD 18-APR-2001.
XX
PF 11-OCT-2000; 2000EP-00308948.
XX
PR 15-OCT-1999; 99JP-00294493.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Ushio S, Nukada Y, Yamamoto K, Kurimoto M;
XX
DR WPI; 2001-275206/29.
XX
DR N-PSDB; AAC85680.
XX
PT New human interleukin-1-related polypeptide and polynucleotide, useful

```

PT for gene therapy and in developing drugs as regulators of natural killer
 PT activity, are capable of inhibiting natural killer activity.
 XX
 XX Claim 1; Page 12; 15pp; English.
 PS
 CC This sequence represents an interleukin-1 (IL-1)-related polypeptide. IL-
 CC 1 related polypeptide was isolated from HRP-MLT cells, FERM-BP-2430, an
 CC established human T-cell line. IL-1 related polypeptide is useful for
 CC inhibiting natural killer (NK) activity, which is related to the immune
 CC system of mammals. The DNA encoding the IL-1 related polypeptide is
 CC useful in gene therapy of patients in need of NK activity inhibition and
 CC others suffering from immunodeficiency
 CC
 XX Sequence 218 AA;
 SQ
 Alignment Scores:
 Pred. No.: 1,34e-93 Length: 218
 Score: 895.00 Matches: 169
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.92% Gaps: 0
 DB: 4 Indels: 0

US-09-869-566-4 (1-650) x AAB47186 (1-218)

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QY 112 CCNAAAGTGAAGAACTTAAACCCGAAAGAAATTGAGATTTCATGACCGAGATCACAAGTA 171
DB 50 ProlysVallyAsnLeuAsnProlyslsPheSerIleHisaspGlnsphislyVal 69
QY 172 CTGGCTCTGAGCTCTGGAGATCTCATAGCAGATTCCAGATAAACAATACATAGCCGAGAG 231
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProaspLysAsnTyrIleArgProGlu 89
QY 232 ATCTCTTTGATTAAGCTCATCTTGAAGTCAAGCTGAGCTGCGGAAAGAAAGTCCGATT 291
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnlysglySerProIle 109
QY 292 CTCCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTCGACAGATTAAGACAAAGT 351
DB 110 LeuLeuGlyValSerlysglyGlnPheCysLeuTyrCysAspLysAspLysGlyInsSer 129
QY 292 CTCCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTCGACAGATTAAGACAAAGT 351
DB 110 LeuLeuGlyValSerlysglyGlnPheCysLeuTyrCysAspLysAspLysGlyInsSer 129
QY 352 CATCCATCCCTTCAGCTGAGAAAGAGAAACATGAAAGCTGGCTGCCAAAGAAATGA 411
DB 130 HisProSerLeuGlnLeuLysGlnLysLeuMetLysLeuAlaAlaGlnLysGlyInsSer 149
QY 412 GCACGCCGGCCCTTCATCTTTTATAGAGGCTCAGGTGGGCTCTGGAACAATGCTGAGTGC 471
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrAsnMetLeuGlnSer 169
QY 472 GCGGCTCACCCCGATGGTTTCATCTGCACTCTGCAATTGATAGAGCTGTGGGGTG 531
DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnProValGlyVal 189
QY 532 ACAGATAAATTTGAGAACAAGAAACATGATTTTTCATTTCACAGATTGGCAAGT 591
DB 190 ThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProValCysLysAla 209
QY 592 GAAATGAGCCCGCATGAGTCAAGCGAT 618
DB 210 GluMetSerProSerGlnValSerAsp 218

RESULT 13
AAG68116
ID AAG68116 standard; protein; 218 AA.
XX AAG68116;
AC
XX
DT 22-JAN-2002 (first entry)
XX
DE Human interleukin 1 family protein SEQ ID NO:2.
XX
KW Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
KW identification.

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XX OS Homo sapiens.
XX PN JP2001231578-A.
XX PD 28-AUG-2001.
XX PF 07-DEC-2000; 2000JP-00372864.
XX PR 09-DEC-1999; 99JP-00349780.
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX DR WPI; 2001-609968/70.
XX DR N-PSDB; AA171179.
XX PT An IL-1 family protein, used for the development of diagnostic and
XX treatment agents.
XX PS Claim 1; Page 30; 38pp; Japanese.
XX SQ Sequence 218 AA;

Alignment Scores:
Pred. No.: 1.34e-93 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: 4 Gaps: 0

US-09-869-566-4 (1-650) x AAG68116 (1-218)

QY 112 CCAAGGTGAAGAACTTAAACCCGAGAAATTGACGATTCAGACGATCAAGTCAAAAGTA 171
DB 50 ProlValValLysAsnLeuAsnProLysPheSerLeuHisAspGlnAspHisLysVal 69
QY 172 CTGGTCTCGGACCTCTGGAGATCTCATAGAGAGTCCGATTAACATCAATAGCCCGAGG 231
DB 70 LeuValLeuAspSerLysAsnLeuLeuAlaValProAspLysAsnTyrTrileArgProGlu 89
QY 232 ATCTTCTTTCGATTACCTCATCTCATCTGAGCTCAGCTCTGCGGAGAAAGAACTCCGATT 291
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySerProIle 109
QY 292 CTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGAGATAAGAGACAAAGT 351
DB 110 LeuLeuGlyValAspSerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129
QY 352 CATCCATCCCTTCAGCTGAAGAGAGAAAGAACTGATGAAGTGGCTGCCCAAAAGGATCA 411
DB 130 HisProSerLeuGlnLeuLysGlyLysGlyLeuMetLysLeuAlaGlnLysGluSer 149
QY 412 GCAAGCGCGGCGCTTCATCTTTTATAGGGCTCAGAGTGGGCTCCGTAACATGCTGAGTGG 471
DB 150 AlaAspArgProPheIlePheTyrAlaGlnValGlySerTrpAsnMetLeuGluSer 169
QY 472 GCGGCTACCCCGGATGGTTTCATCTGACCTCTGCAATTGATGAAGCTGTGGGGTG 531
DB 170 AlaAlaHisProGlyTyrPheIleCysTrpSerCysAsnGlyAsnGluProValGlyVal 189
QY 532 ACGAGTAATTTTGAAGAACAGAAACATGATTTTTCATTTTAAACGATTTGCAAGCT 591
DB 190 ThrAspLysPheGlnAsnArgLysHisLysGluPheSerPheGlnProValCysLysAla 209
QY 592 GAAATGAGCCCGCAGTGAAGTCAAGCGAT 618
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```
DB 210 GluMetSerProSerGluValSerAsp 218
RESULT 14
ID AAB85136 standard; protein; 218 AA.
AC AAB85136;
XX
DB 22-AUG-2001 (first entry)
DE Interleukin-1 homologue (IL-1H4) polypeptide.
XX
XX Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
XX immunosuppressive; antipruritic; antialbtritic; cytostatic; antiHIV;
XX cerebroprotective; antiaesthetic; vasotropic; vulnary; osteopahic;
XX immunostimulant; antiatherosclerotic; nootropic; neuroprotective;
XX gene therapy; vaccine.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
FT Peptide 1..20
FT Cleavage-site /note= "signal peptide" 20..21
FT Protein 21..218
FT /note= "specifically claimed mature protein (AAB85138)"

XX PN WO200140247-A1.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US032521.
XX PR 01-DEC-1999; 99US-00452140.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Kumar S, McDonnell PC, Young PR;
XX DR WPI; 2001-389949/41.
XX DR N-PSDB; AAF84120.
XX PT Novel Interleukin-1 homologue, IL-1H4, for treating chronic and acute
PT inflammation, septicemia, autoimmune diseases, transplant rejection,
PT graft versus host disease, stroke, ischemia, allergy and asthma.
XX PS Example; Page 29; 30pp; English.
XX
XX The invention provides an isolated interleukin-1 homologue, IL-1H4
XX polypeptide. The IL-1H4 polypeptide can be expressed by standard
XX recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
XX modulators are useful for treating chronic and acute inflammation,
XX septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
XX psoriasis and arthritis), transplant rejection, graft versus host
XX disease, infection, stroke, ischemia, acute respiratory disease syndrome,
XX allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
XX osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
XX heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
XX polynucleotides are useful as diagnostic reagents and for chromosome
XX identification. The present sequence represents the IL-1H4 polypeptide
XX
XX Sequence 218 AA;

Alignment Scores:
Pred. No.: 1.34e-93 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: 4 Gaps: 0

US-09-869-566-4 (1-650) x AAB85136 (1-218)
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QY 112 CCMAAGGTGAAGACTTAAACCCGAAGAAATTGACATTGATGACCAAGATGACAAAGTA 171
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 QY 172 CTGGTCTCTGGAATCTCGGAATCTCAGAGAGATTCCAGATAAACATACATAGCCCAAG 231
 DB 70 LeuValIleuAspSerGlyAsnLeuIleAlaValProAspIysAsnIylIleArgProGlu 89
 QY 232 ATCTTCTTTGACATTACCTCATCTTCATGAGCTGAGCTGCGGAGAAAGATCCGATT 291
 DB 90 IlePhePheAlaIleuAlaSerSerIleuSerSerAlaSerAlaGlnIylsGlySerProIle 109
 QY 292 CTCCTGGGGGTCTCTTAAAGGGAGTTTGTCTTACTGACAGATTAAGACAAAT 351
 DB 110 LeuLeuGlyValSerIylsGlyIuPheCysLeuIylrCysAspIysAspIylsGlyIuSer 129
 QY 352 CATCCATCCCTCAGTGAAGAAAGAGAACTGATGAGCTGCGCAAAAGAAATCA 411
 DB 130 HisProSerLeuGlnIleuIylsGlyIuPheCysLeuMetIylsLeuAlaIleGlnIylsGlyIuSer 149
 QY 412 GCACGCCGCCCTTCACTTTTATAGAGGCTCAGGTGGGCTCCTGAAACATGCTGAGATCG 471
 DB 150 AlaArgArgProPheIlePheIylrArgAlaGlnValGlySerTrpAsnMetIleuGlyIuSer 169
 QY 472 GCGGCTCACCCGGATGTTTCATCTGACCTCTGCAATTGATGAGCTGTGGGGTG 531
 DB 170 AlaAlaHisProGlyTrpPheIleCysThrSerCysAsnGlnIuProValGlyVal 189
 QY 532 ACAGATAAATTGAGAACAGGAAACATTTGATTTTCAACAGATTGGCAAGGT 591
 DB 190 ThrAspIylsPheGlnAsnArgIylsHisIleGlnIylsPheGlnProValCysIylsAla 209
 QY 592 GAAATGAGCCCCAGTGAAGTCAAGCAT 618
 DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 15
 ADJ88306
 ID ADJ88306 standard; protein; 218 AA.
 XX

ADJ88306;

06-MAY-2004 (first entry)

Human interleukin-1zeta protein variant.

Interleukin-1zeta; gene therapy; immune system; haematopoietic cell;

inflammatory disorder; infection; allergy; cancer; human.

Homo sapiens.

Location/Qualifiers

30..41 "EpiTope"

45..50 "EpiTope"

46..60 "EpiTope"

107..113 "EpiTope"

156..167 "EpiTope"

163..169 "EpiTope"

163..169 "EpiTope"

163..169 "EpiTope"

163..169 "EpiTope"

163..169 "EpiTope"

163..169 "EpiTope"

PA (SCHE) SCHERING CORP.
 XX
 XX Timans JC;
 PI
 XX
 DR WPI: 2004-189656/18.
 DR N-PSDB; ADJ88305.
 XX
 PT New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
 PT useful for diagnosing, preventing or treating diseases associated with
 PT abnormal expression of interleukin, e.g. inflammation, infection or
 PT cancer.
 XX
 PS Claim 2; SEQ ID NO 4; 36bp; English.
 XX
 CC The invention relates to an isolated or recombinant nucleic acid encoding
 CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.
 CC The composition and methods are useful in diagnosing or treating
 CC degenerative or abnormal conditions which directly or indirectly involve
 CC development, differentiation or function, e.g. of the immune system
 CC and/or haematopoietic cells. The invention may also be used for
 CC preventing or treating other diseases or disorders associated with
 CC abnormal expression or triggering of response to the interleukin, such as
 CC inflammatory disorders, infection, allergies or cancer. The present
 CC sequence is human interleukin-1zeta variant.
 XX
 SQ Sequence 218 AA;

Alignment Scores:

Pred. No.:	1,34e-93	Length:	218
Score:	895.00	Matches:	169
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.92%	Indels:	0
DB:	8	Gaps:	0

US-09-869-566-4 (1-650) x ADJ88306 (1-218)

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 DB 50 ProlysValIlysAsnLeuAsnProIylsPheSerIleHisAspGlnAspHisIylsVal 69
 QY 172 CTGGTCTCTGGAATCTCGGAATCTCAGAGAGATTCCAGATAAACATACATAGCCCAAG 231
 DB 70 LeuValIleuAspSerGlyAsnLeuIleAlaValProAspIysAsnIylIleArgProGlu 89
 QY 232 ATCTTCTTTGACATTACCTCATCTTCATGAGCTGAGCTGCGGAGAAAGATCCGATT 291
 DB 90 IlePhePheAlaIleuAlaSerSerIleuSerSerAlaSerAlaGlnIylsGlySerProIle 109
 QY 292 CTCCTGGGGGTCTCTTAAAGGGAGTTTGTCTTACTGACAGATTAAGACAAAT 351
 DB 110 LeuLeuGlyValSerIylsGlyIuPheCysLeuIylrCysAspIysAspIylsGlyIuSer 129
 QY 352 CATCCATCCCTCAGTGAAGAAAGAGAACTGATGAGCTGCGCAAAAGAAATCA 411
 DB 130 HisProSerLeuGlnIleuIylsGlyIuPheCysLeuMetIylsLeuAlaIleGlnIylsGlyIuSer 149
 QY 412 GCACGCCGCCCTTCACTTTTATAGAGGCTCAGGTGGGCTCCTGAAACATGCTGAGATCG 471
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 DB 170 AlaAlaHisProGlyTrpPheIleCysThrSerCysAsnGlnIuProValGlyVal 189
 QY 532 ACAGATAAATTGAGAACAGGAAACATTTGATTTTCAACAGATTGGCAAGGT 591
 DB 190 ThrAspIylsPheGlnAsnArgIylsHisIleGlnIylsPheGlnProValCysIylsAla 209
 QY 592 GAAATGAGCCCCAGTGAAGTCAAGCAT 618
 DB 210 GluMetSerProSerGluValSerAsp 218

Search completed: May 28, 2005, 17:35:18
Job time : 95 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 28, 2005, 17:23:16 ; Search time 39.5 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	895	78.9	218	3	US-09-233-125-2	Sequence 2, Appl1
2	895	78.9	218	4	US-09-398-1128-4	Sequence 4, Appl1
3	863.5	76.1	218	4	US-09-398-1128-2	Sequence 2, Appl1
4	702	61.9	167	3	US-09-128-155-7	Sequence 7, Appl1
5	702	61.9	178	3	US-09-128-155-2	Sequence 2, Appl1
6	693	61.3	136	3	US-09-128-155-11	Sequence 11, Appl1
7	623	54.9	115	3	US-09-128-155-5	Sequence 5, Appl1
8	623	54.9	115	3	US-09-128-155-9	Sequence 9, Appl1
9	623	54.9	115	3	US-09-128-155-13	Sequence 13, Appl1
10	473.5	41.8	185	3	US-09-128-155-18	Sequence 18, Appl1
11	229.5	20.2	169	2	US-08-750-032-2	Sequence 2, Appl1
12	229.5	20.2	169	3	US-09-069-619-2	Sequence 2, Appl1

13	229.5	20.2	169	3	US-09-494-018-2	Sequence 2, April 1
14	229.5	20.2	169	4	US-09-398-4128-15	Sequence 15, April 1
15	229	20.2	157	4	US-09-976-472A-2	Sequence 2, April 1
16	212	18.7	158	4	US-09-970-033-8	Sequence 13, April 1
17	212	18.7	158	4	US-09-970-033-8	Sequence 13, April 1
18	191.5	16.9	156	4	US-09-398-4128-13	Sequence 5, April 1
19	174.5	15.4	155	3	US-09-417-455-5	Sequence 5, April 1
20	174.5	15.4	155	3	US-09-348-942-5	Sequence 5, April 1
21	174.5	15.4	155	3	US-09-316-081-5	Sequence 5, April 1
22	174.5	15.4	155	3	US-09-578-458-5	Sequence 5, April 1
23	174.5	15.4	155	3	US-09-522-964A-5	Sequence 5, April 1
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25	174.5	15.4	155	4	US-09-576-008-5	Sequence 5, April 1
26	174.5	15.4	155	4	US-09-949-016-6827	Sequence 6827, April 1
27	174.5	15.4	187	4	US-09-949-016-6356	Sequence 9356, April 1
28	171	15.1	160	4	US-09-398-4128-14	Sequence 14, April 1
29	167	14.7	178	3	US-09-000-630C-21	Sequence 21, April 1
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32	167	14.7	178	3	US-09-348-942-9	Sequence 9, April 1
33	167	14.7	178	4	US-09-457-626-9	Sequence 9, April 1
34	167	14.7	178	4	US-09-576-008-9	Sequence 9, April 1
35	165.5	14.6	152	3	US-09-578-458-18	Sequence 18, April 1
36	162	14.3	176	4	US-09-949-016-6468	Sequence 8468, April 1
37	161	14.2	180	1	US-08-476-860-13	Sequence 13, April 1
38	161	14.2	180	1	US-08-910-733-13	Sequence 13, April 1
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ALIGNMENTS

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RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293.625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-293-625-2

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Alignment Scores:		
Pred. No.:	5,49e-99	length: 218
Score:	895.00	Matches: 169
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
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QY	292	CTCTGGGGGATCTCTAAAGGGGAGTTTGTCTCTACTGTGCAAGAGATMAAGCAAAAGT	351
Db	110	IleuLeuGluValaSerIysGlyGluPheCysLeuTyrCysAspIysAspIysGlyGlnSer	129
QY	352	CATCCATCCCTTACGCTGAAGAGAGAAACTGATGAAAGCTGGCTGCCCAAAAGAAATCA	411
Db	130	HisProSerIeuGlnIeuNlysGlyIuIysLeuMetCysLeuAlaAlaGluIysGlnSer	1498
QY	412	GCACGGCGGGCCCTTCATCTTTTAATAGGGGTGACAGGGGGCTCCGTGGAAATCATCTGAGACG	471
Db	150	AlaIArgIArgProPheIleIlePheTyrAlaAlaGlnValGlySerTTPAspMetLeuGlnSer	165
QY	472	GGCGCTCACCCCGAGATGTTTCATCTTGCACTCTCCCAATGTATGATGAGCTGTGGGGTG	531
Db	170	AlaAlaHisProGlyIyrPheIleIecysThrIserCysAsnGlyAlaProValGlyVal	189
QY	532	ACGATATAATTTGAGAACAGGAAACACATTTGAATTTTCATTTCAACCGATTTCGAAAGCT	591
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QY	592	GAAATGAGCCCCAGTAGAGGTACGGCAT	618
Db	210	GluMetSerProSerGluValaIserAsp	218

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Db      110 LeuLeuGlYvalSerIysGlYIuPheCysIeuYrCYsaEplYsaEplYsGlYGlInSer 129
QY      352 CATCCATCCCTTCAGCTGTAAGAAGGAAACATGATGAAGCTGGCTGCCCAAAAGCAATCA 411
Db      130 HisProSerIeuGlInIeuYsIysGlYIusIeuMetYsIeuAlaIaIaGlInLYsGlInSer 149
QY      412 GCAGCGCGGCGCTTATCTTTATATAGGGCTCAGGCGGGCTCCTGGAACATGCTGAGTGC 471
Db      150 AlaArgArgProPheIlePheYrArgIaIaGlInValGlySerTrpIasnMetIeuGlInSer 165
QY      472 GCGGCTCACCCCGGATGGTTCATCTGCACCTTCCTGCAATTGAAATGAGCCTGTGGGCTG 531
Db      170 AlaAlaHisProCooLYrPheIleCYsIhrSerCYsaEncYsaEngIuProValGlyVal 189
QY      532 ACAGATAAATTTGAGAAACAGAAACACATGAAATTTTCATTTCAACACAGTTTGGAAGCT 591
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QY      592 GAATGAGCGCCGAGTGAGTCAAGCAT 618
Db      210 GluMetSerProSerGluValSerasp 218

RESULT 3
US-09-398-412B-2
: Sequence 2, Application US/09398412B
: Patent No. 6680380
: GENERAL INFORMATION:

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RESULT 2
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; Sequence 4, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; TITLE OF INVENTION: methods
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-4

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; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reagents
; TITLE OF INVENTION: methods
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-2

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Db          16 AspTGTGluTyrAspGlnProGlnTyrCysCysLeuGlnAspProTlaaGlySerProLeuGln 35

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US-09-869-566-4 (1-650) X US-09-398-412B-4 (1-218)

QY 106 AGAGTCCA-----

QY 112 CCAAGGTGAGAACTTAACCCGAGAAATTCAGCATTCATGACCAGATCACAAGTA 171

Db 36 ProGlyProSerLeuProThrMetAsnPheValHisThrSerArgLysValLysSerLeu 55

Db 50 ProlysValLysAsnLeuAsnProLysLysPheSerIleHisAspGlnAspHisLysVal 69

130 AACCGAAGAAATTCAGCATTCATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGG 189

172 CTGGTCTGGACTCTGGAACTCATAGCAGTTCAGATAAACTACATACGCCCAGAG 231

Db 56 AspProLysLysPheSerIleH1sAspGlnAspHisValLeuValLeuAspSerGly 75

Db 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89

190 AATCTCATAGCAGTTCAGATAAAATCACTACGCCAGAGATCTCTTGCATTAGCC 243

232 ATCTTCTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGGAGTCCGATTT 291

16 AsnLeuLeaIaValProAspPlyAsnIyrIeaGrProGluIePhePheAlaLeuAla 33

Db 90 ILePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluGlySerProIle 105

250 TCACTTGAGCTCAGCCCTCTCGGAGAAAGGAGTCCGATCTCTCGGGCTCCTAA 307

292 C T C C T G G G G T C T C T A A G G G A G T W T G T C T C T A C T G A C A A G G A T A A G G A C A A G T 351

96 seiseleuserseiraadgindlyseleuieueueuglyvalseuys 11

QY 310 GGGAGTTTGTCTACTGTGACAAAGATAAAGCAAAAGTCAATCCCTTCAGCTG 369
DB 116 GtlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSerHisProSerLeuGlnLeu 135
QY 370 AAGAAAGAAATCTGATGAAGCTGCTGCCAAAGAAATCAGACGCCGCCCTTCATC 429
DB 136 LysLysGlnLysLeuMetLysLeuAlaGlnLysGlnSerLysAlaArgProPheile 155
QY 430 TTTTATAGGGCTCAGGTGGGCTCTCGAATCATGCTGAGAGCGCGGCTCAGCCCGATG 489
DB 156 PheTyrAlaGlnValGlySerAlaGlnSerAlaAlaHisProGlyTyr 175
QY 490 TTCACTGCACTCTCTGCAATTTGTAATGAGCCCTGTGGGCTGACAGATAATTGAGAAC 549
DB 176 PheileCysThrSerCysAsnGlySerAlaGlyValThrAspLysPheGlnLeu 195
QY 550 AAGAAACACATTTGATTTTCATTTTCAACACATTTGCAAAAGCTGAAATGAGCCCGATGAG 609
DB 196 ArgLysHisIleGlnPheSerPheGlnProValCysLysAlaGlnMetSerProSerGln 215
QY 610 CTCAGGAT 618
DB 216 ValSerAsp 218
RESULT 4
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-7
Alignment Scores:
Pred. No.: 8,88e-76 Length: 167
Score: 702.00 Matches: 131
Percent Similarity: 97.14% Conservative: 5
Best Local Similarity: 93.57% Mismatches: 4
Query Match: 61.90% Indels: 0
DB: 3 Gaps: 0
US-09-869-566-4 (1-650) x US-09-128-155-7 (1-167)
QY 199 GCAGTTCAGATTAATAACTACATACGCCCGAGATCTTTGCAATTAAGCTTCATCTTG 258
DB 28 SerLeuProThrMetAsnPheValHisThrLysIlePhePheAlaLeuAlaSerSerLeu 47
QY 259 AGCTCAGCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGTCTCTAAAGGGAGTTT 318
DB 48 SerSerAlaSerAlaGlnLysGlySerProIleLeuLeuGlyValSerLysGlyGlnPhe 67
QY 319 TGTCTCTACTGTGACAAAGATAAAGCAAAAGTCAATCCCTTCAGCTGAAAGAGAG 378
DB 68 CysLeuTyrCysAspLysAspLysGlyGlnSerHisProSerLeuGlnLeuLysGln 87
QY 379 AACTGATGAGCTGGCTGCCCAAAAGAAATGACAGCGCGGCTTCATCTTTATAGG 438
DB 88 LysLeuMetLysLeuAlaIleGlnLysGlnSerAlaArgProPheIlePheTyrArg 107

QY 439 GCTCAGTGGGCTCTGGAACATGCTGAGTGGCGGCTCACCCCGATGTTTCATCTGC 498
DB 108 AlaGlnValGlySerTrpAsnMetLeuGlnSerAlaAlaHisProGlyTyrPheileCys 127
QY 499 ACCTCTGCAATTTGATATAGCTGTGGGCTGACAGATAATTGAGAAACAGAAACAC 558
DB 128 ThrSerCysAsnGlySerAlaGlnProValGlyValThrAspLysPheGlnLysArgLysHis 147
QY 559 ATTGAATTTTCATTTCAACACATTTGCAAAAGCTGAAATGAGCCCGATGAGGTCAGCGAT 618
DB 148 IleGlnPheSerPheGlnProValCysLysAlaGlnMetSerProSerGlnValSerAsp 167
RESULT 5
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2
Alignment Scores:
Pred. No.: 9,12e-76 Length: 178
Score: 702.00 Matches: 131
Percent Similarity: 97.14% Conservative: 5
Best Local Similarity: 93.57% Mismatches: 4
Query Match: 61.90% Indels: 0
DB: 3 Gaps: 0
US-09-869-566-4 (1-650) x US-09-128-155-2 (1-178)
QY 199 GCAGTTCAGATTAATAACTACATACGCCCGAGATCTTTGCAATTAAGCTTCATCTTG 258
DB 39 SerLeuProThrMetAsnPheValHisThrLysIlePhePheAlaLeuAlaSerSerLeu 58
QY 259 AGCTCAGCTCTGCGGAGAAAGAAAGTCCGATTTCTCTGGGGGTCTCTAAAGGGAGTTT 318
DB 59 SerSerAlaSerAlaGlnLysGlySerProIleLeuLeuGlyValSerLysGlyGlnPhe 78
QY 319 TGTCTCTACTGTGACAAAGATAAAGCAAAAGTCAATCCCTTCAGCTGAAAGAGAG 378
DB 79 CysLeuTyrCysAspLysAspLysGlyGlnSerHisProSerLeuGlnLeuLysGln 98
QY 379 AACTGATGAGCTGGCTGCCCAAAAGAAATGACAGCGCGGCTTCATCTTTATAGG 438
DB 99 LysLeuMetLysLeuAlaIleGlnLysGlnSerAlaArgProPheIlePheTyrArg 118
QY 439 GCTCAGTGGGCTCTGGAACATGCTGAGTGGCGGCTCACCCCGATGTTTCATCTGC 498
DB 119 AlaGlnValGlySerTrpAsnMetLeuGlnSerAlaAlaHisProGlyTyrPheileCys 138
QY 499 ACCTCTGCAATTTGATATAGCTGTGGGCTGACAGATAATTGAGAAACAGAAACAC 558
DB 139 ThrSerCysAsnGlySerAlaGlnProValGlyValThrAspLysPheGlnLysArgLysHis 158
QY 559 ATTGAATTTTCATTTCAACACATTTGCAAAAGCTGAAATGAGCCCGATGAGGTCAGCGAT 618
DB 159 IleGlnPheSerPheGlnProValCysLysAlaGlnMetSerProSerGlnValSerAsp 178

RESULT 6
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

Alignment Scores:
Pred. No.: 5,69e-75 Length: 136
Score: 695.00 Matches: 130
Percent Similarity: 98.52% Conservative: 3
Best Local Similarity: 96.30% Mismatches: 2
Query Match: 61.29% Indels: 0
DB: Gaps: 0
US-09-869-566-4 (1-650) x US-09-128-155-11 (1-136)

QY 214 AACTACATACGCCAGATCTTCTTGATAGCTCATCTTGAGCTCAGGCTCTGGG 273
DB 2 AaapheVHieThrlrYsilePhepheaLeuAlaSerSerleuSerSerAlaSerAla 21
QY 274 GAGAAAGAGATCCGATCTCCGAGGAGTCTTAAGGAGGAGTTTGTCTACTGTGAC 333
DB 22 GluysGlySerProIleuLeuGlyValSerlyGlyGluPheCysLeuTyrcysasp 41
QY 334 AAGATTAAGACAAAGTATCCATCCCTTCACTAGCTAAGAGAGAACTGATGAAGCTG 393
DB 42 LysAspLyGlyGlnSerHisProSerleuGlnLeuLyGlyGluSerleuMetLysleu 61
QY 394 GCTGCCCAAAAGAAATCAGACGCGCGCTTCATCTTTATAGGCTCAGGTGGGCTCC 453
DB 62 AlaAlaGlnLyGlnSerAlaArgArgProPheIlePheTyArgAlaGlnValGlySer 81
QY 454 TGAACATGCTGAGTCCGCGGCTCACCCCGATGTTGATCGACCTCGCAATTGT 513
DB 82 TTPaerMetLeuGlnSerAlaAlaHisProGlyTTPheIleCysHisSerCysaency 101
QY 514 AATGAGCTGTGGGTGACAGATTAATTGAGACAGAAACACATTGATTTTCATT 573
DB 102 AaengluProValGlyValThrAspLysPheGluAsnArgLysHisIleGluPheSerPhe 121
QY 574 CAACGATTTGCAAGCTGAATGAGCCCGAGTGAAGCTGAGCGAT 618
DB 122 GlnProValCysLyAlaGlnMetSerProSerGluValSerasp 136

RESULT 7
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

Alignment Scores:
Pred. No.: 2.52e-66 Length: 115
Score: 623.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.94% Indels: 0
DB: Gaps: 0
US-09-869-566-4 (1-650) x US-09-128-155-5 (1-115)

QY 274 GAGAAAGAGATCCGATCTCCGAGGAGTCTTAAGGAGGAGTTTGTCTACTGTGAC 333
DB 1 GluysGlySerProIleuLeuGlyValSerlyGlyGluPheCysLeuTyrcysasp 20
QY 334 AAGATTAAGACAAAGTATCCATCCCTTCACTAGCTAAGAGAGAACTGATGAAGCTG 393
DB 21 LysAspLyGlyGlnSerHisProSerleuGlnLeuLyGlyGluSerleuMetLysleu 40
QY 394 GCTGCCCAAAAGAAATCAGACGCGCGCTTCATCTTTATAGGCTCAGGTGGGCTCC 453
DB 41 AlaAlaGlnLyGlnSerAlaArgArgProPheIlePheTyArgAlaGlnValGlySer 60
QY 454 TGAACATGCTGAGTCCGCGGCTCACCCCGATGTTGATCGACCTCGCAATTGT 513
DB 61 TTPaerMetLeuGlnSerAlaAlaHisProGlyTTPheIleCysHisSerCysaency 80
QY 514 AATGAGCTGTGGGTGACAGATTAATTGAGACAGAAACACATTGATTTTCATT 573
DB 81 AaengluProValGlyValThrAspLysPheGluAsnArgLysHisIleGluPheSerPhe 100
QY 574 CAACGATTTGCAAGCTGAATGAGCCCGAGTGAAGCTGAGCGAT 618
DB 101 GlnProValCysLyAlaGlnMetSerProSerGluValSerasp 115

RESULT 8
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-9

Alignment Scores:
Pred. No.: 2.52e-66 Length: 115
Score: 623.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.94% Indels: 0
DB: 3 Gaps: 0
US-09-869-566-4 (1-650) x US-09-128-155-9 (1-115)
QY 274 GAGAAAGAAAGTCCGATTCCTCGGGGGTCTTAAAGGAGATTGTTCTCTACTGTGAC 333
Db 1 GtLysGlySerProIleuLeuGlyValSerIleGlyGluPheCysLeuTyrCysAsp 20
QY 334 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAGAAAGAAAGAACTGATGAGCTG 333
Db 21 LysAspIleGlyGlnSerHisProSerIleuLeuLysIleGlyGluPheMetIleu 40
QY 394 GGTGCCCAAAAGGAAATCAGACGCCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 453
Db 41 ALaAlaGlnLysIleuSerAlaAlaHisProGlyTyrPheIleCysThrSerCysAnCys 60
QY 454 TGGAAATGCTGAGTCCGGCGCTCAACCCGAGTGGTTCATCTGACCTCTGCAATTGT 513
Db 61 TrpAsnMetLeuGlnSerAlaAlaHisProGlyTyrPheIleCysThrSerCysAnCys 80
QY 514 AATGACCTGTGGGTGACAGATAAATTGAGAACAGAAACATGTAATTTGATT 573
Db 81 AsnGlnProValGlyValThrAspLysPheGluAsnArgLysHisIleGluPheSerPhe 100
QY 574 CAACGATTGCAAAAGCTGAAATGAGCCCGAGTGAAGTCAGCCAT 618
Db 101 GlnProValCysLysAlaGluMetSerProSerGluValSerAsp 115
RESULT 9
US-09-128-155-13
Sequence 13, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-13
Alignment Scores:
Pred. No.: 2,52e-66 Length: 115
Score: 623.00 Matches: 115
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 54.94% Indels: 0
DB: 3 Gaps: 0
US-09-869-566-4 (1-650) x US-09-128-155-13 (1-115)
QY 274 GAGAAAGAAAGTCCGATTCCTCGGGGGTCTTAAAGGAGATTGTTCTCTACTGTGAC 333
Db 1 GtLysGlySerProIleuLeuGlyValSerIleGlyGluPheCysLeuTyrCysAsp 20
QY 334 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAGAAAGAAAGAACTGATGAGCTG 333
Db 21 LysAspIleGlyGlnSerHisProSerIleuLeuLysIleGlyGluPheMetIleu 40
QY 394 GGTGCCCAAAAGGAAATCAGACGCCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 453

Db 41 ALaAlaGlnLysIleuSerAlaAlaHisProPheIlePheTyrArgAlaGlnValGlySer 60
QY 454 TGGAAATGCTGAGTCCGGCGCTCAACCCGAGTGGTTCATCTGACCTCTGCAATTGT 513
Db 61 TrpAsnMetLeuGlnSerAlaAlaHisProGlyTyrPheIleCysThrSerCysAnCys 80
QY 514 AATGACCTGTGGGTGACAGATAAATTGAGAACAGAAACATGTAATTTGATT 573
Db 81 AsnGlnProValGlyValThrAspLysPheGluAsnArgLysHisIleGluPheSerPhe 100
QY 574 CAACGATTGCAAAAGCTGAAATGAGCCCGAGTGAAGTCAGCCAT 618
Db 101 GlnProValCysLysAlaGluMetSerProSerGluValSerAsp 115
RESULT 10
US-09-128-155-18
Sequence 18, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 185
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: synthetically generated
LOCATION: (1)...(185)
OTHER INFORMATION: human sequence predicted using an alignment algorithm which
OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(185)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18
Alignment Scores:
Pred. No.: 3,18e-48 Length: 185
Score: 473.50 Matches: 90
Percent Similarity: 94.90% Conservative: 3
Best Local Similarity: 91.84% Mismatches: 4
Query Match: 41.75% Indels: 1
DB: 3 Gaps: 1
US-09-869-566-4 (1-650) x US-09-128-155-18 (1-185)
QY 244 TTAGCCTCATCTTGAAGTCAAGCTCTCGGAGAAAGAAAGTCCGATTCCTCGGGGCTC 303
Db 71 LeuSerSerLeuGlnArgSerAlaSerAlaGlnLysGlySerProIleuLeuGlyVal 90
QY 304 TCTAAAGGAGAGTTTGTCTTACTGTGACAGATAAAGAAAGAAAGTCAATCCCTT 363
Db 91 SerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSerHisProSerIleu 110
QY 364 CAGCTGAAGAGAGAAAGTGAAGCTGCGCCCAAAAGAAATCAGACCGCGGCC 423
Db 111 GlnLeu---LysGlnLysLeuMetLysLeuAlaAlaGlnLysGlnSerAlaArgAspPro 129
QY 424 TTCAATCTTTATAGGCTCAGGTGGGCTCTGGAACATGCTGAGTCCGCGCTCAACCC 483
Db 130 PheIlePheTyrArgAlaGlnValGlySerTrpAsnMetLeuGlnSerAlaAlaHisPro 149

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QY      484 GGAATGCTTCAATCGACCCCTGGCAGATTGTAAATGAGCCGTGGGGTGACAGAT 537
        |||
DB      150 GIIYTPHellecysThrserysaEncysasnglprvalGIyle***asn 167

RESULT 11
; Sequence 2, Application US/08790032
US-08-790-032-2
; Patent No. 5863769
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
; TITLE OF INVENTION: Beta (IL-1RA_)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,032
; FILING DATE: 28-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5031
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-790-032-2

Alignment Scores:
Pred. No.:          7.73e-19           Length:          169
Score:              229.50             Matches:          56
Percent Similarity: 53.12%             Conservative:    29
Best Local Similarity: 35.00%           Mismatches:     62
Query Match:       20.24%               Indels:         13
DB:                2                   Gaps:            5

US-08-869-566-4 (1-650) x US-08-790-032-2 (1-169)
QY      64 GACGATGACGACAAGCTTGGCGCGGGAATTGACTTCCTTTGCAGAGGTCCAAAGTGAAG 123
        |||
DB      7 AAPALASPGLyGIyglYArGlAvalTYrGlnSerwecyslys----- 21
QY      124 AACTTAACCCGAGAAGAAATTCAGCATTCATGACCAGATCACAAAGTACTGTCTTGAC 183
        |||
DB      22 -----ProtlehrIGlyThrIleAsnAspLeuasnInclnValTrpThrlEuGln 38
QY      184 TCTGGAATCTCATPACGAGTTCAGATAAAAACCTACATACGCCOAGAGATCTTCTTGCA 243
        |||
DB      39 GIylGlnAsnIeuValAlvalPrArGserAspservalThrPrvalAlthrValAlval 58
QY      244 TTAGCCTCATCCTTAGAGCTAGGCTCTGCGGAG---AAAGAGAGTCCGATTCCTCGGGG 300
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Db      55  ILeThCybLyTyTyrProGluAlaLeuInGlnIyHrGglYAspProIleTyRLeuGly 78
QY      301  GHTCTAAAGGGAGAGTTTGTCTACTGTGAACAAGATAAAGACAAGTCAATCC 360
      ::: ||||| ||||| ||||| |||||
Db      79  ILeGlnAspProGluMetCysLeuTyTyCysGlnYsValGlyGlnGln-----ProThr 96
QY      361  CTTGACGTGAAGAAGAGAACTGATGAAGCGGTGGTCCCAAGAAAGATACGACGCCGG 420
      ||||| ||||| ::||| ||||| ||||| |||||
Db      97  LeGlnIleuYsGlnGlnIlyIsIleMetAspLeuTyRyGlyGlnPProGluProVal---Lys 115
      ||||| ||||| ::||| ||||| ||||| |||||
QY      421  CCCCTCATTTTATAGAGCTCAGGTGGCTCTCGGAACATGCTGGAAGTCGGCGGCTCAC 480
      ||||| ::||| ::||| ||||| ||||| |||||
Db      116  ProHeuLeuPheTyRyRglYalYsThrGlyHrGlyThrSerThrLeuGlnSerValAlaPhe 135
      ||||| ::||| ::||| ||||| ||||| |||||
QY      481  CCCGATGGTTGATCTGCACCTCTCGCAATGTTATAGCTGTGGGGGTCAGCATAA 540
      ||||| ||||| ::||| ||||| ||||| |||||
Db      136  ProAspTrpPheIleAlaSerSer---LysArgAspGlnProIleIleuThrSerGln 154
      ||||| ||||| ::||| ||||| ||||| |||||

RESULT 12
US-09-069-619-2
/ Sequence 2, Application US/09069619
/ Patent No. 6054559
/ GENERAL INFORMATION:
/ APPLICANT: Young, Peter and Lisa Marshall
/ TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
/ TITLE OF INVENTION: Beta (IL-1RA_)
/ NUMBER OF SEQUENCES: 2
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19406-0939
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/069,619
/ FILING DATE: Herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/007,464; and 08/790,032
/ FILING DATE: filed 14-JAN-1998; and 28-JAN-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Han, William, T.
/ REGISTRATION NUMBER: 34,344
/ REFERENCE/DOCKET NUMBER: AT50051-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5219
/ TELEFAX: 610-270-5090
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 169 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-069-619-2

Alignment Scores:
Pred. No.: 7.73e-19
Score: 229.50
Percent Similarity: 53.12%
Best Local Similarity: 35.00%
Query Match: 20.24%
DB: 3 Gaps: 5

US-09-869-566-4 (1-650) x US-09-069-619-2 (1-169)

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QY 64 GACGATGACGACAAAGCTTGGCGCGCGGAATTAGCTCTTTGACAGAGCTCCAAAGTGAAG 123
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Db 7 AapAlaAspGlyGlyValArgAlaValIYrgInserMeCylys----- 21
QY 124 AACTTAACCCGAGAAATTCAGATTGACACGACGATCAAAAGTACTGCTCTGAC 183
|||
Db 22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnGlnValIleThrLeuGln 38
QY 184 TCTGGGAATCTCATAGAGTTCAGATTAATAACTATACAGCCGACAGATCTTTTGGCA 243
|||
Db 39 GlyGlnAsnLeuValAlaValIleProArgSerAspSerValIleThrProValIleValAlaVal 58
QY 244 TTAGCCTCATCTTGAAGCTCAGCTCGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300
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Db 59 IleThrCysLeuTyProGlnIleAsnGlnGlnIleValIleAspProIleTyLeuGly 78
QY 301 GCTCTTAAGGAGAGTTTGTCTCTACTGTGACAAAGATTAAGAGCAAAATCATCTCC 360
|||
Db 79 IleGlnAsnProGlnIleCysLeuTyProGlnIleValIleGlnIle-----ProThr 96
QY 361 CTTGAGCTGAAGAGAGAACTGATGAAGCTGCTGCCCAAAAGATCAGACGCGG 420
|||
Db 97 LeuGlnIleuAsnGlnIleuAsnIleuMetAspLeuTyArgIleProGlnProValIle---Lys 115
QY 421 CCCTTCATCTTTATAGGCTCAGCTGAGCTCCTGGAACATGCTGAGTGGCGGCTCAC 480
|||
Db 116 ProPheLeuPheTyArgAlaIleTyThrGlyArgThrSerThrLeuGlnSerValAlaIlePhe 135
QY 481 CCGGATGCTTATCTGACCTCTGCAATTGTAATGAGCTGTTGGGCTGACAGATAA 540
|||
Db 136 ProAspTrpPheIleAlaSerSer---LysArgAspGlnProIleIleLeuThrSerGln 154

RESULT 13
US-09-494-018-2

/ Sequence 2, Application US/09494018
/ Patent No. 639573
/ GENERAL INFORMATION:
/ APPLICANT: Peter R. Young
/ TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST BETA
/ TITLE OF INVENTION: (IL-1RAB)
/ FILE REFERENCE: ATG-50051-D1
/ CURRENT APPLICATION NUMBER: US/09/494, 018
/ CURRENT FILING DATE: 2000-01-28
/ EARLIER APPLICATION NUMBER: 09/069, 619
/ EARLIER FILING DATE: 1998-04-29
/ EARLIER APPLICATION NUMBER: 09/007, 464
/ EARLIER FILING DATE: 1998-01-14
/ EARLIER APPLICATION NUMBER: 08/790, 032
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 169
/ TYPE: PRT
/ ORGANISM: HOMO SAPIENS
US-09-494-018-2

Alignment Scores:
Pred. No.: 7,73e-19 Length: 169
Score: 229.50 Matches: 56
Percent Similarity: 53.12% Conservative: 29
Best Local Similarity: 35.00% Mismatches: 62
Query Match: 20.24% Indels: 13
Gaps: 5

US-09-869-566-4 (1-650) x US-09-494-018-2 (1-169)
QY 64 GACGATGACGACAAAGCTTGGCGCGCGGAATTAGCTCTTTGACAGAGTCCAAAGTGAAG 123
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Db 7 AapAlaAspGlyGlyValArgAlaValIYrgInserMeCylys----- 21

QY 124 AACTTAACCCGAGAAATTCAGATTGACACGACGATCAAAAGTACTGCTCTGAC 183
|||
Db 59 IleThrCysLeuTyProGlnIleAsnGlnGlnIleValIleAspProIleTyLeuGly 78

Db 22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnGlnValIleThrLeuGln 38
QY 184 TCTGGGAATCTCATAGAGTTCAGATTAATAACTATACAGCCGACAGATCTTTTGGCA 243
|||
Db 39 GlyGlnAsnLeuValAlaValIleProArgSerAspSerValIleThrProValIleValAlaVal 58
QY 244 TTAGCCTCATCTTGAAGCTCAGCTCGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300
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Db 59 IleThrCysLeuTyProGlnIleAsnGlnGlnIleValIleAspProIleTyLeuGly 78
QY 301 GCTCTTAAGGAGAGTTTGTCTCTACTGTGACAAAGATTAAGAGCAAAATCATCTCC 360
|||
Db 79 IleGlnAsnProGlnIleCysLeuTyProGlnIleValIleGlnIle-----ProThr 96
QY 361 CTTGAGCTGAAGAGAGAACTGATGAAGCTGCTGCCCAAAAGATCAGACGCGG 420
|||
Db 97 LeuGlnIleuAsnGlnIleuAsnIleuMetAspLeuTyArgIleProGlnProValIle---Lys 115
QY 421 CCCTTCATCTTTATAGGCTCAGCTGAGCTCCTGGAACATGCTGAGTGGCGGCTCAC 480
|||
Db 116 ProPheLeuPheTyArgAlaIleTyThrGlyArgThrSerThrLeuGlnSerValAlaIlePhe 135
QY 481 CCGGATGCTTATCTGACCTCTGCAATTGTAATGAGCTGTTGGGCTGACAGATAA 540
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Db 136 ProAspTrpPheIleAlaSerSer---LysArgAspGlnProIleIleLeuThrSerGln 154

RESULT 14
US-09-398-412B-15

/ Sequence 15, Application US/09398412B
/ Patent No. 6680380
/ GENERAL INFORMATION:
/ APPLICANT: Timans, Jacqueline C.
/ TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reager
/ TITLE OF INVENTION: methods
/ FILE REFERENCE: DX0904K
/ CURRENT APPLICATION NUMBER: US/09/398, 412B
/ CURRENT FILING DATE: 1999-09-17
/ PRIOR APPLICATION NUMBER: US 60/100948
/ PRIOR FILING DATE: 1998-09-18
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15
/ LENGTH: 169
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-398-412B-15

Alignment Scores:
Pred. No.: 7,73e-19 Length: 169
Score: 229.50 Matches: 56
Percent Similarity: 53.12% Conservative: 29
Best Local Similarity: 35.00% Mismatches: 62
Query Match: 20.24% Indels: 13
Gaps: 5

US-09-869-566-4 (1-650) x US-09-398-412B-15 (1-169)
QY 64 GACGATGACGACAAAGCTTGGCGCGCGGAATTAGCTCTTTGACAGAGTCCAAAGTGAAG 123
|||
Db 7 AapAlaAspGlyGlyValArgAlaValIYrgInserMeCylys----- 21

QY 124 AACTTAACCCGAGAAATTCAGATTGACACGACGATCAAAAGTACTGCTCTGAC 183
|||
Db 22 -----ProIleThrGlyThrIleAsnAspLeuAsnGlnGlnValIleThrLeuGln 38
QY 184 TCTGGGAATCTCATAGAGTTCAGATTAATAACTATACAGCCGACAGATCTTTTGGCA 243
|||
Db 39 GlyGlnAsnLeuValAlaValIleProArgSerAspSerValIleThrProValIleValAlaVal 58
QY 244 TTAGCCTCATCTTGAAGCTCAGCTCGCGAG--AAAGAAAGTCCGATTCTCTGCGG 300
|||
Db 59 IleThrCysLeuTyProGlnIleAsnGlnGlnIleValIleAspProIleTyLeuGly 78

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QY 301 GTCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGCAAAATCATTCATCC 360
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QY 79 IEGlnAsnProGlnuMetCysLeuIYrCysGluYValGlyGluIn-----ProThr 96
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 CTTGACCTTAAGAGAGAAAGTGAAGTGGCTGCCCAAAAGAAATCAGACGCCCG 420
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 97 LeuGlnLeuIYsGlnuIYsIleMetAspLeuIYrGlyGlnProGlnProVal--Lys 115
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 CCCTTCATCTTTTATAGCTGAGTGGGCTCTCGAATCATGTGGAGTGGCGGCTCAC 480
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 116 ProPheLeuPheIYrThrGlnAlaYsThrGlyArgThrSerThrLeuGlnSerValAlaPhe 135
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 481 CCCGATGCTTCATCTGACCTCTCTGCAATTTGATAGCTGTGTGGGCTGACAGATAA 540
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 ProAspTrpPheIleAlaSerSer--LysArgAspGlnProIleIleLeuThrSerGln 154
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15

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US-09-976-472A-2
; Sequence 2, Application US/0976472A
; Patent No. 675166
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: RENSCHAW, Blair R.
; TITLE OF INVENTION: IL-1 ETA DNA AND POLYPEPTIDES
; FILE REFERENCE: 2932-B
; CURRENT APPLICATION NUMBER: US/09/976,472A
; PRIOR APPLICATION NUMBER: PCT/US00/14435
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/162,331
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/135,758
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 157
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-976-472A-2
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Alignment Scores:
Pred. No.: 8.61e-19 Length: 157
Score: 229.00 Matches: 47
Percent Similarity: 59.26% Conservative: 33
Best Local Similarity: 34.81% Mismatches: 51
Query Match: 20.19% Indels: 4
DB: 4 Gaps: 3
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US-09-869-566-4 (1-650) x US-09-976-472A-2 (1-157)

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QY 133 CGAAGAAATTCAGCATTCATGACGAGATCACAAATGACTGCTCCTGGACTCTGGGAAT 192
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QY 9 ProLysSerIYrAlaIleArgAspSerArgGlnMetValTrpValIleuSerGlyAsnSer 28
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 193 CTCATAGCAGTTCAGATAAAATCAATACGCCAGAGATCTTCTTTCGATTAGCC-- 249
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 29 LeuIleAlaIleProIleuSerArgSerIleIYsProValThrIleuHisIleuIleAlaCys 48
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 250 TCATCTTGAGCTCAGCCTCTGCGAGAAAGAAAGATTCCTCTGGGGGTCTCTAA 309
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 49 ArgAspThrGlnPheSerAspLysGlnIYsGlyAsnMetValIYrIleuGlyIleIYsGly 68
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 310 GGGGATTTTGTCTCTACTGTGACAAAGATTAAGCAAAAGTCAATCCCTTCAGCTG 369
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 69 LysAspLeuIYsLeuPheCysAlaGlnIleGlnGlyLys-----ProThrIleuGlnLeu 86
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 370 AAGAAGAGAGAAATCGATGAAGCTGCTGCCAAAGAAATCATGACGCGGCGCTTCATC 429
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 87 LysGlnIYsAsnIleMetAspLeuIYrValGlnIYsLys---AlaGlnIYsProPheLeu 105
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 430 TTTTATAGGCTCAGGTGGCTCTCTGGAACATGCTGGAGTGGCGGCTCACCCCGATGG 489
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 106 PhePheHisAsnIYsGlnGlySerThrSerValPheGlnSerValSerIYrProGlyTrp 125
QY 490 TTCATCTGCACCTCTCTGCAATTTGATGAGCCTGTTGGGGTGACA 534
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 126 PheIleAlaThrSerThrThrSerGlyGlnProIlePheLeuThr 140
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: May 28, 2005, 17:41:22
Job time : 42.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM nucleic - protein search, using frame_plus_r2p model

Run on: May 28, 2005, 17:20:26 ; Search time 30 Seconds
(without alignments)
4169.393 Million cell updates/sec

Title: US-09-869-566-4
Perfect score: 1134
Sequence: 1 tcaatcacatgctcgcact.....cgactctagagatcccgcg 650

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=PIR_79 -QPMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09869566@CN_1_1_38@runac_27052005_163131_19922 -NCPU=6 -ICPU=3
-NO_WMAP -LANG=QUEYER -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -NMAP TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	174.5	15.4	155	2	JC7104 interleukin-1 rece
2	167	14.7	178	2	A44610 interleukin-1 rece
3	161	14.2	180	2	A39386 interleukin-1 rece
4	158.5	14.0	177	2	A30368 interleukin-1 rece
5	154.5	13.6	177	2	A54377 interleukin-1 rece
6	146.5	12.9	178	2	C40956 interleukin-1 rece
7	135.5	11.9	267	2	S36373 interleukin-1 beta
8	131.5	11.6	266	1	S23010 interleukin-1 beta
9	121.5	10.7	267	1	JN0724 interleukin-1 beta
10	120.5	10.6	269	1	I55969 interleukin-1 beta
11	118	10.4	266	1	IC8018 interleukin-1 beta
12	98	8.6	269	1	IC801B interleukin-1 beta
13	95.5	8.4	246	2	B25528 trypsin (EC 3.4.21
14	92.5	8.2	268	1	A30584 interleukin-1 beta

15	91	8.0	404	2	S34031 KTR3 protein - yea
16	89.5	7.9	214	2	JC5646 interleukin-1 beta
17	89.5	7.8	1250	1	B45219 N-methyl-D-asparta
18	88	7.7	466	2	T33574 hypothetical prote
19	84	7.4	270	1	ICMS1 interleukin-1 alph
20	84	7.4	432	2	S41956 interleukin-1 Sch
21	83.5	7.4	776	2	S67053 hypothetical prote
22	83	7.3	845	2	T17291 trypsin (EC 3.4.21
23	82.5	7.3	246	1	TRRT1 hypothetical prote
24	82.5	7.2	393	2	E70767 probable flavoproc
25	82.5	7.3	513	2	T37806 molybdenum cofacto
26	81	7.0	320	2	A81434 NADH dehydrogenase
27	81	7.0	686	2	B87490 hypothetical prote
28	81	7.1	914	2	B96592 trypsin (EC 3.4.21
29	80.5	7.1	246	1	TRRT2 B120 protein - hum
30	80.5	7.0	1142	2	T00022 conserved hypotet
31	79.5	6.9	510	2	A42750 conserved hypotet
32	79.5	7.0	740	2	F71369 hypothetical prote
33	79.5	6.9	1357	2	T29265 hypothetical prote
34	79	6.9	682	2	F83228 hypothetical prote
35	78.5	6.9	244	2	F90419 cytosol aminopepti
36	78	6.9	493	2	A87459 hypothetical prote
37	78	6.9	1277	2	E70224 otogelin - mouse
38	78	6.8	2910	2	T42214 probable protein s
39	77.5	6.8	426	2	C75297 probable s/t prote
40	77.5	6.7	490	2	E71486 K-CI cotransport p
41	77.5	6.7	757	2	T16149 58k membrane-assoc
42	77.5	6.8	1116	2	T31432 myocyte-specific e
43	77	6.7	427	2	A53798 hypothetical prote
44	77	6.7	507	2	S25831
45	77	6.8	859	2	C87358

ALIGNMENTS

RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C/Species: Homo sapiens (man)
C/Date: 03-Dec-1999 #seqname_revision 03-Dec-1999 #text_change 09-Jul-2004
R/Mulero, J.J.; Pace, A.M.; Nelken, S.T.; Joeb, D.B.; Correa, T.R.; Drmanac, R.; Ford, J.
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A>Title: IL1H1: A novel interleukin-1 receptor antagonist gene.
A/Reference number: JC7104; MUID:99443727; PMID:10512743
A/Cross-references: UNIPROT:Q9UBH0; GB:AF186094; NID:G6049804; PIDN:AAF02757.1; PID:G6045
A/Accession: JC7104
A/Molecule type: mRNA
A/Residues: 1-155 <MULT>
C/Genetics:
A/Map position: 2q14
C/Keywords: macrophage

Alignment Scores:

Pred. No.:	1,45e-09	Length:	155
Score:	174.50	Matches:	54
Percent Similarity:	42.60%	Conservative:	18
Best Local Similarity:	31.95%	Mismatches:	48
Query Match:	15.39%	Indels:	49
DB:	2	Gaps:	7

US-09-869-566-4 (1-650) x JC7104 (1-155)	
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DB 4 SerGlyAlaLeuCys-----	
QY 151 CATGACCAAGATCAACAAGTACTGTCTCGACTCTGGGAATTCATATGACAGTTCCAGAT 210	
DB 12 LysAaSpSerAlaLeuValLeuTyrlleuHisAaAaGlnLeu-----	
QY 211 AAAAAGTACATACGCGCCGAGAGATCTTCTTTCATAGCTACCTTTCAGCTCAGCTCT 270	

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Db 27 -----LeuAlaGlyLeuHisAlaGlyLys 35
QY 271 GCGGAAAGGA-----AGT 285
Db 36 ValIleIleValGluGluIleSerValValProSerArgTrpLeuAspAlaSerLeuSer 55
QY 286 CCGATTCTCTGGGGGCTCTTAAAGGGAGATTGTTCTCTACTGTGACAAAGATAAGGA 345
Db 56 ProValIleLeuGlyValGlnGlySerGlnCysLeuSerCys-----GlyValGly 73
QY 346 CAAAGTCATCCATCCCTTTCAGCTGGAAGAGAAACTATGAGTGT---GCTGCCAA 402
Db 74 Gln---GluProThrLeuThrLeuGluProValAsnIleMetGluLeuTyrLeuGlyAla 92
QY 403 AAGGAATGACAGACGCGCCCTTCATCTTTATAGAGGCTTCAGGTGGGCTCTGGAACATG 462
Db 93 LysGluSer-----LysSerPheThrPheTyrArgArgAspMetCylLeuThrSerSer 110
QY 463 CTGAGTGTGGGGCTGACCCCGAGATGTTTCATCTGCACCTCTGCAATTGTATGAGCT 522
Db 111 PheGluSerAlaAlaTyrTrpProGlyTrpPheLeuCysThrValProGluAlaAspGlnPro 130
QY 523 GTTGGGTGACAGATTAATTGAGAAC 549
Db 131 ValArgLeuThrGlnLeuProGluAsn 139

RESULT 2
A44610
Interleukin-1 receptor antagonist precursor - mouse
M:Alternate names: IL-1Ra
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A44610; BA0956; A49031; I56106; I52970
R:Matsumura, H.; Rousnel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A:Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophag
A:Reference number: A44610; MUID:91316273; PMID:1830498
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MAT>
A:Cross-references: UNIPROT:P25085; GB:M64404; NID:G198236; PIDN:AAA3277.1; PID:G198297
R:Reisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.U.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A:Reference number: A40956; MUID:91271363; PMID:1828896
A:Accession: BA0956
A:Molecule type: DNA
A:Residues: 7-178 <BIS>
A:Cross-references: GB:M63100; NID:G198389; PIDN:AAA39310.1; PID:G198390
R:Shuck, M.E.; Bessaly, T.E.; Tracey, D.E.; Blenkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A:Title: Cloning, heterologous expression and characterization of murine interleukin 1
A:Reference number: A49031; MUID:92037824; PMID:1834470
A:Accession: A49031
A:Molecule type: mRNA
A:Residues: 23-178 <SHU>
A:Cross-references: GB:S64082; NID:G238584; PIDN:AA20265.1; PID:G238585
A:Experimental source: peritoneal macrophages, ICR strain
A>Note: sequence extracted from NCBI backbone (NCIN:64082, NCBI:P:64085)
R:Zahedi, K.; Seidlin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A:Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mappin
A:Reference number: I56106; MUID:91250712; PMID:1828262
A:Accession: I56106
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-178 <RES>
A:Cross-references: GB:M74294; NID:G198387; PIDN:AAA39309.1; PID:G198388
R:Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A:Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A:Reference number: I52970; MUID:94271931; PMID:8003626

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A:Accession: I52970
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-178 <RE2>
A:Cross-references: GB:I32838; NID:G487864; PIDN:AAA20576.1; PID:G528978
C:Genetics:
A:Gene: IL-1rn
A:Introns: 40/2; 70/1; 107/3
C:Superfamily: interleukin-1
C:Keywords: cytokine receptor
F:1-26/Domain: signal sequence #status predicted <SIG>
F:127-178/Product: interleukin-1 receptor antagonist #status predicted <MA2>

Alignment Scores:
Pred. No.: 8.72e-09 Length: 178
Score: 167.00 Matches: 51
Percent Similarity: 46.95% Conservative: 26
Best Local Similarity: 31.10% Mismatches: 75
Query Match: 14.73% Indels: 12
DB: 2 Gaps: 7

US-09-869-566-4 (1-650) x A44610 (1-178)
QY 91 AATTGAGCTCTTGGAGAGGTCGCAAGGTGAAGACTTAAACCGAAGAAATTCAGACT 150
Db 22 SerGluAlaAlaCysArgProSerGlyLysArgProCysLysMetGlnAlaPheArgIle 41
QY 151 CATGACACAGATCAAAAGTACTGCTGCTGACCTCGGAATTCATGACAGTCCAGAT 210
Db 42 TrpAspTrpArgGlnIleThrPheTyrLeuArgAsnGlnIleAla----- 58
QY 211 AAAAACAATACATACG---CCAGAGATCTTCTTGCATTAGCTCCTTACCTTACAGTCC 267
Db 59 ---GlyTyrLeuGlnGlyProAsnIle-----LysLeuGluGluLysIleAspMetVal 75
QY 268 TCTGGGAGAAAGAAAGTCCATCTCTCGGGGGCTCTAAAGGGAGCTTTGTCTCTAC 327
Db 76 ProIleAspLeuHisSer---ValPheLeuGlyIleHisGlyLysLysLeuCysLeuSer 94
QY 328 TGTGACAAAGATTAAGACAAAGTATCATCCATCCCTGACCTGAGAGAGAACTGATG 387
Db 95 CysAlaIleLysSerGlyAspAspIle-----LysLeuGlnLeuGluValAsnIleThr 112
QY 388 AAGCTGCTGCCCAAAAGAAATACAGACGCGCGCTTCATCTTTATAGGCTCAGGTG 447
Db 113 AspLeuSerLysAsnIleGluGluLysArg---PheThrPheIleArgSerGluLys 131
QY 448 GGCCTCTGGAACATGCTGAGTCGGCGGCTCACCCCGATGTTGATCTGCACCTCTGC 507
Db 132 GlyProThrThrSerPheGluSerAlaAlaCysProGlyTrpPheLeuCysThrThrLeu 151
QY 508 AATTGTAATGAGCTGTGGGTGACAGATTAATTGAGAACAGAAACACATT---GAA 564
Db 152 GluAlaAspArgProValSerLeuThrAsnThrProGluGluProLeuIleValThrLys 171
QY 565 TTTTCATTTCAA 576
Db 172 PheTyrPheGln 175

RESULT 3
A33386
Interleukin-1 receptor antagonist, long intracellular splice form - human
N:contains: interleukin-1 receptor antagonist, short intracellular splice form
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
A:Accession: I37893; A39386
R:Munzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Mantovani
J. Exp. Med. 182, 623-628, 1995
A:Title: Cloning and characterization of a new isoform of the interleukin 1 receptor ant
A:Reference number: I37893; MUID:9555865; PMID:7629520
A:Accession: I37893
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA

```

[illegible]

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:

A:Reference number: A40956; MUID:91271363; PMID:1828896

A:Accession: A40956

A:Molecule type: DNA

A:Residues: 1-177 <EIS>

A:Cross-references: UNIPROT:PI8510; GB:M63099; NID:G186385; PIND:AA41943.1; PID:G186386

R:Renard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Soctney, H.; Sheer, D.; Solari, R.

Cytokine 4, 83-89, 1992

A:Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist gene

A:Reference number: 137894; MUID:92338323; PMID:1385987

A:Accession: 137894

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-177 <LEN>

A:Cross-references: EMBL:X64532; NID:G33798; PIND:CAA45832.1; PID:G33799

R:Cartier, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J.

J.G.; Siou, L.C.; Hardie, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrichson, R.L.; Tr

Nature 344, 633-638, 1990

A:Title: Purification, cloning, expression and biological characterization of an interle

A:Reference number: A50368; MUID:90220867; PMID:2139180

A:Accession: A50368

A:Molecule type: mRNA

A:Residues: 1-177 <CAR>

A:Note: parts of this sequence, including the amino end of the mature protein, were confi

R:Rienberg, S.P.; Evans, R.J.; Arend, W.P.; Verdier, B.; Brewer, M.T.; Hannum, C.H.; T

Nature 343, 341-346, 1990

A:Title: Primary structure and functional expression from complementary DNA of a human tr

A:Reference number: S08160; MUID:90136921; PMID:2137201

A:Accession: S08160

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-177 <E12>

A:Cross-references: GB:X52015; NID:G32576; PIND:CAA3262.1; PID:G32577

R:Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joellin, F.G.; Dripps, D.J.; Helmdal, P.L.; Arn

Nature 343, 336-340, 1990

A:Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.

A:Reference number: S08159; MUID:90136920; PMID:2137200

A:Accession: S08159

A:Molecule type: protein

A:Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>

R:Bienkowski, M.J.; Bessalu, T.E.; Berger, A.E.; Trusedell, S.E.; Shelly, J.A.; Laborde,

J. Biol. Chem. 265, 14505-14511, 1990

A:Title: Purification and characterization of interleukin 1 receptor level antagonist p

A:Reference number: A37822; MUID:90354444; PMID:2143761

A:Accession: A37822

A:Molecule type: protein

A:Residues: 26-52;70-77;122-127;170-175 <BIE>

A:Experimental source: culture medium, PMA-stimulated THP-1 cells

C:Comment: For an alternative splice form, see PIR:A39386

C:Gene: GDB:IL1RN

A:Cross-references: GDB:125897; OMIM:147679

A:Map position: 2q14.2-2q14.2

A:Introns: 39/2; 69/1; 106/3

C:Superfamily: interleukin-1

C:Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein

F:1-35/Domains: signal sequence #status predicted <SIG>

F:126-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>

F:109/Binding site: carbohydrate (Asn) (covalent) #status experimental

Alignment Scores:

Pred. No.:	6,53e-08	Length:	177
Score:	158.50	Matches:	43
Percent Similarity:	48.67%	Conservative:	30
Best Local Similarity:	28.67%	Mismatches:	66
Query Match:	13.98%	Indels:	11
DB:	2	Gaps:	6

US-09-869-566-4 (1-650) x A30368 (1-177)

91 AATTGAGCTCTTGGACGAGGTCCAAAGGTGACGAAGACTTAAACCCGAGAAATTCAGCAATT 150

```

Db      21 SerGluThrIleCysArgProSerGlyArgLysSerIleMetGlnAlaPheArgIle 40
      21  :::::|||||:::|||||:::
Qy      151 CATTGACAGATGATCAACAGTACTGCTGCTGAGCTCGGAGATCTCATACAGTCCAGAT 210
      151  |||||:::|||||:::|||||:::
Db      41 TPAPsValAsnGlnIleThrPheTyrlleuArgAsnGlnIleValAla----- 57
      41  |||||:::|||||:::|||||:::
Qy      211 AAAAATCATATGACG---CCAGAGATCTTCTTGATGATGACCCATCTTGAGCTCAGCC 267
      211  |||||:::|||||:::|||||:::
Db      58 ---GlyTyrIleuGlnIleProAsnVal-----AsnIleuGlnIleuIleAspValVal 74
      58  |||||:::|||||:::|||||:::
Qy      268 TCTGCGGAGAAAGAAAGTCCGATTCCTCTGGGGGCTCTAAAGGGAGTTTGTCTTAC 327
      268  |||||:::|||||:::|||||:::
Db      75 ProIleGluProHisAla---LeuPheIleuGlyIleHISGlyGlyMetCysIleuSer 93
      75  |||||:::|||||:::|||||:::
Qy      328 TGTGACAGATGATTAAGACAAAGTATCCATCCCTTCACTGAGAAAGAGAAACGTGAG 387
      328  |||||:::|||||:::|||||:::
Db      94 CysValIleuSerGlyAspIleuThrArg-----LeuGlnIleuGlnAlaValAsnIleThr 111
      94  |||||:::|||||:::|||||:::
Qy      388 AAGCTGCTGCCCAAGAAAGATGACGACGCGGCTTCATCTTTATAGGGCTCAGTG 447
      388  |||||:::|||||:::|||||:::
Db      112 AspleuSerGluAsnArgLysGlnAspLysArg---PheAlaPheIleArgSerAspSer 130
      112  |||||:::|||||:::|||||:::
Qy      448 GGCTCTCGAATGCTGAGTGGCGGCTCAACCCGAGTGTTCATCTGACCTTCCTGC 507
      448  |||||:::|||||:::|||||:::
Db      131 GlyProThrThrSerPheGluSerAlaIleAlaCysProGlyTyrPheIleuCysThrAlaMet 150
      131  |||||:::|||||:::|||||:::
Qy      508 AATTGTAATGAGCTTGGGGTGACAGAT 537
      508  |||||:::|||||:::|||||:::
Db      151 GluAlaAspGlnProValSerIleuThrAsn 160
      151  |||||:::|||||:::|||||:::

```

RESULT 5

```

A54377
Interleukin-1 receptor antagonist secreted form precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A54377; I46729
R/Cominelli, F.; Borcolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A/Title: Rabbit interleukin-1 receptor antagonist. Cloning, expression, functional chara
A/Reference number: A54377; PMID:94165101; PMID:7509813
A/Accession: A54377
A/Molecule type: mRNA
A/Residues: 1-177 <COM>
A/Cross-references: UNIPROT:P26890; GB:S68977; NID:G545740; PIDN:AAB30093.1; PID:G545741
A/Experimental source: colon tissue
A/Note: Sequence extracted from NCBI backbone (NCBIN:144168, NCBIPI:144163)
R/Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Maeda
Immunology 77, 235-244, 1992
A/Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. Pro
A/Reference number: I46729; PMID:93052512; PMID:1427977
A/Accession: I46729
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-177 <GOT>
A/Cross-references: GB:D21832; NID:G425787; PIDN:BAA04860.1; PID:G452205
C/Superfamily: Interleukin-1
C/Keywords: cytokine receptor; extracellular protein; glycoprotein
F1-25/Domain: signal sequence #status predicted <SIG>
F109/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Alignment Scores:

```

Pred. No.: 1 68e-07 Length: 177
Score: 154.50 Matches: 44
Percent Similarity: 41.10% Conservatve: 23
Best Local Similarity: 26.99% Mismatches: 51
Query Match: 13.62% Indels: 45
DB: 2 Gaps: 6

```

US-09-869-566-4 (1-650) x A54377 (1-177)

```

Qy      103 TGCAGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTGACATTCATGACCGAGAT 162
      103  |||||:::|||||:::|||||:::

```

```

Db      25 CysArgProSerGlyLysArgProCysArgMetGlnAlaPheArgIleTPAspValAsn 44
      25  |||||:::|||||:::|||||:::
Qy      163 CACAAAGTACTGCTGCTGAGCTCGGAGATCTCATAGCA----- 201
      163  |||||:::|||||:::|||||:::
Db      45 GlnIleThrPheTyrlleuArgAsnGlnIleValAlaGlyTyrIleuGlnIleProAsn 64
      45  |||||:::|||||:::|||||:::
Qy      202 -----GTTCCAGATTAATAAATCATATGACCCAGAGATC 234
      202  |||||:::|||||:::|||||:::
Db      65 AlaIleuGlnIleuGlnIleAspValIlePro-----LeuGlnProGlnIleu 80
      65  |||||:::|||||:::|||||:::
Qy      235 TTCTTGATTAAGCTTCATCTTGAGCTCAGCTCTCGGAGAAAGAAAGTCCGATTCCTC 294
      235  |||||:::|||||:::|||||:::
Db      81 LeuPhe----- 82
      81  |||||:::|||||:::|||||:::
Qy      295 CTGGGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAG-----GATTAAGACAA 348
      295  |||||:::|||||:::|||||:::
Db      83 LeuGlyIleGlnArgGlyLysIleuCysIleuSerCysValIleuSerGlyAspIleuMetLys 102
      83  |||||:::|||||:::|||||:::
Qy      349 AGTCATCCATCCCTTCAGCTGAGAAAGAAACTGATGAAGCTGCTGCCCAAGAA 408
      349  |||||:::|||||:::|||||:::
Db      103 LeuHis-----LeuGlnAlaValAsnIleThrAspLeuGlyLysAsnLysGln 118
      103  |||||:::|||||:::|||||:::
Qy      409 TCAGACAGCCGCGCTTCATCTTTATAGGGCTCAGTGGCTCCTGGAACATGCTGAG 468
      409  |||||:::|||||:::|||||:::
Db      119 GlnAspLysArg---PheThrPheIleArgSerAsnSerGlyProThrThrPheGln 137
      119  |||||:::|||||:::|||||:::
Qy      469 TCGGGGGCTCACCCGAGATGTTTCATGTCACCTCGCAATGTAATGAGCTGTGGG 528
      469  |||||:::|||||:::|||||:::
Db      138 SerAlaSerCysProGlyTyrPheIleuCysThrAlaLeuGlnAlaAspGlnProValSer 157
      138  |||||:::|||||:::|||||:::
Qy      529 GTGACAGAT 537
      529  |||||:::|||||:::|||||:::
Db      158 LeuThrAsn 160
      158  |||||:::|||||:::|||||:::

```

RESULT 6

```

C40956
Interleukin-1 receptor antagonist precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C/Accession: C40956
R/Bissenberg, S.B.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A/Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A/Reference number: A40956; PMID:91271363; PMID:1828896
A/Accession: C40956
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-178 <EIS>
A/Cross-references: UNIPROT:P25086; GB:M63101; NID:G204928; PIDN:AAA41434.1; PID:G204929
C/Superfamily: Interleukin-1
C/Keywords: cytokine receptor

```

Alignment Scores:

```

Pred. No.: 1 12e-06 Length: 178
Score: 146.50 Matches: 47
Percent Similarity: 39.55% Conservatve: 23
Best Local Similarity: 26.55% Mismatches: 58
Query Match: 12.92% Indels: 49
DB: 2 Gaps: 6

```

US-09-869-566-4 (1-650) x C40956 (1-178)

```

Qy      100 CTTGACAGATGATCAAGGTGAAGAACTTAAC----- 132
      100  |||||:::|||||:::|||||:::
Db      3 TleCysArgGlyProTyrSerHisIleuIleSerIleuLeuIleuLeuPheArgSer 22
      3  |||||:::|||||:::|||||:::
Qy      133 -----CCGAGAA-----TTCAGCATTCAT 153
      133  |||||:::|||||:::|||||:::
Db      23 GluSerAlaGlyHisProAlaGlyLysArgProCysLysMetGlnAlaPheArgIleTyr 42
      23  |||||:::|||||:::|||||:::
Qy      154 GACCAAGATCAACAAGTACTGCTCTGACCTCGGAAATCTATAGCA----- 201
      154  |||||:::|||||:::|||||:::
Db      43 AspThrAsnGlnIleuThrPheTyrlleuArgAsnGlnIleuIleAlaGlyTyrIleuGln 62
      43  |||||:::|||||:::|||||:::

```

```

OY 202 -----GTTCCAGATATAAACTACATACGCCAGATCTTCTTGATTA 246
      ::::: ||| ||| |||
Db 63 GlyProanthrilyleuGlulysIleAspMetValProIleAspHe----- 79
OY 247 GCCTCATCTTGAGCTCAGCCTCTGCGGAGAAAGAAAGATCTCTCTGGGGCTCT 306
      ::::: ||| ||| |||
Db 80 -----ArganValPheleuGlulIleHis 87
OY 307 AAAGGAGATTGTCTCTACTGTGACAAAGATAAAGACAAAGTCAATCCCTTCAG 366
      |||::: ||| ||| |||
Db 88 GlyGlyLysleuYsleuSerCysValLysSerGlyAspAspThr-----LysleuGln 105
OY 367 CTGAAGAGAGAGAAATGAACTGAGCTGCGCCCAAAAGATCAGACGCGGCCCTTC 426
      |||::: ||| ||| |||
Db 106 LeuGlulGluValAsnIleThrAspLeuAsnLysGluLysAspArg---Phe 124
OY 427 ATCTTTATATAGGCTCAGCTGCGGCTCTGACACATCTGTGAGCTGCGCGCTCA 486
      |||::: ||| ||| |||
Db 125 ThrPheIleArgSerGluThrGlyProThrThrSerPheGluSerleuAlaCysProGly 144
OY 487 TGGTTATATGCACTCTCCGCAATTGTATGACCTCTTGGGGTGACAGAT 537
      |||::: ||| ||| |||
Db 145 TTPheLeuCysThrThrleuGluAlaAspHisProValSerleuThrAsn 161

RESULT 7
S38373
Interleukin-1 beta precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: S38373
R/Vandenbroeck, K.; Fiteu, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde
Bur, J. Biochem. 217, 45-52, 1993
A/Title: Gene sequence, cDNA construction, expression in Escherichia coli and genetrical
A/Reference number: S38373; MUID:94039070; PMID:8223584
A/Accession: S38373
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-267 <VAN>
A/Cross-references: UNIPROT:Q29082; EMBL:X4566; NID:9407899; PIDN:CAA52660.1; PID:94079
C/Genetics:
A/Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C/Superfamily: Interleukin-1

Alignment Scores:
Pred. No.: 1,6e-05 Length: 267
Score: 135.50 Matches: 51
Percent Similarity: 48.30% Conservative: 34
Best Local Similarity: 28.98% Mismatches: 75
Query Match: 11.95% Indels: 16
Db: 2 Gaps: 8

US-09-869-566-4 (1-650) x S38373 (1-267)
OY 12 GTCTGCACTTGTGATCTAGCTCTTGTGAGCTGAGTTGCTGACTACAAAGACATGA 71
      ||||| ||||| ||| ::||| ::|||
Db 83 ValCysAspAspSerProlySerIlePheSer-SerVal-----PheGluGluGlu 100
OY 72 CGACAGACTTGGGCC---GCCAATTCACTCTTTGACAGAGCTCAAGAGTGAAGAACTT 128
      ||||| ||||| ||| ::||| ::|||
Db 100 olleValleuGluLysIleAlaAsnGlyPheleuCysAspAlaThrProValGlnSerVal 120
OY 129 AAACCCGAAGAAATTGACATTCATGACCAAGATCAAAAGTACTGTCTCTGACCTTGG 188
      ::||| ||| ::||| ||| ||| ||| |||
Db 120 LaspCysLys-----LeuGlnAspLysAspGluLysAlaLeuValleuAlaLysPr 137
OY 189 GAATCATGAGCAGTTCAGAT-----AAAACTACATAGCCGCCAGAGATCTTCTTCG 242
      ::||| ||| ||| ||| ||| ||| |||
Db 137 ohIseGluLeuLysAlaLeuHisleuLeuLysGlyAspLeuLysArgGluValAlaPheCys 157
OY 243 ATTAGCTCATCTTGAGCTCAGCTTCGCGAGAAAGAAAGTCCGATTCCTCTGGGGGAT 302
      ::||| ||| ::||| ||| ||| ||| |||
Db 157 smetSerPheValGlnGlyAspAspSerAspAspLys---IleProValThrleuGlyL 176

```

```

OY 303 CTCTAAAGGAGATTGTCTCTACTGT---GACAAAGATATAAGACAAAGTCAATCC 359
      : ||| ||| ||| ||| |||
Db 176 elysGlyLysAsnleuTyrlleuSerCysValMetLysAsp-----AspThrProh 193
OY 360 CCTTCACTGTAAGAGAGAAACTGATGAACTGCTGCGCCCAAAAGATTCAGACGCCG 419
      |||::: ||| ||| ||| |||
Db 193 rleuGlnleu-----GluAspValAspProlySerTyrrProlyAspArgAspMetGlu 211
OY 420 GCCCTTCACTTTATATAGGCTCAGCTGCGGCTCTGGAACATGCTGAGTCCGGCTCA 479
      : |||::: ||| ||| ||| |||
Db 211 sArgPheValAlaPheTyrlLysThrGluLysAsnArgValGluPheGluSerAlaLeuTy 231
OY 480 CCCCAGATGATTCATCTGACCTCTGCAATGTATGTAAGCTCTGT 525
      |||::: ||| ||| ||| |||
Db 231 rProanthrilylIleSerThrSerGlnAlaGluGlnLysProVal 246

RESULT 8
S23010
Interleukin-1 beta precursor - sheep
N/Alternate names: hematopoietin-1; IL-1 beta
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C/Accession: S23010; S43047; S13092; B61246
R/Seow, H.F.; Rochel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A/Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.
A/Reference number: S23010; MUID:92119335; PMID:1840515
A/Accession: S23010
A/Molecule type: mRNA
A/Residues: 1-266 <SE0>
A/Cross-references: UNIPROT:P21621; EMBL:X56972; NID:91808; PIDN:CAA40293.1; PID:91809
A/Note: the sequence from Fig. 1 is inconsistent with that from Fig. 2 in having an addit
R/Sargan, D.R.
submitted to the EMBL Data Library, May 1992
A/Reference number: S43047
A/Accession: S43047
A/Molecule type: mRNA
A/Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <SAR>
A/Cross-references: EMBL:X54796; NID:91273; PIDN:CAA58566.1; PID:91274
R/Fiskerstrand, C.; Sargan, D.
Nucleic Acids Res. 18, 7165, 1990
A/Title: Nucleotide sequence of ovine interleukin-1 beta.
A/Reference number: S13092; MUID:91088326; PMID:2263490
A/Accession: S13092
A/Molecule type: mRNA
A/Residues: 1-13, 'C', 15-54, 'K', 56-61, 'S', 63, 'A', 65-144, 'L', 146-266 <PIS>
A/Cross-references: EMBL:X54796
A/Note: the authors translated the codon AGT for residue 62 as Arg
R/Andrew, A.E.; Barcham, G.J.; Brandon, M.R.; Nash, A.D.
Immunology 74, 453-460, 1991
A/Title: Molecular cloning and characterization of ovine IL-1alpha and IL-1beta.
A/Reference number: A61246; MUID:92120716; PMID:1769692
A/Accession: B61246
A/Molecule type: mRNA
A/Residues: 1-144, 'L', 146-266 <AND>
A/Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C/Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a)
C/Genetics:
A/Gene: IL-1-beta
C/Superfamily: Interleukin-1
C/Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F/114-266/Product: Interleukin-1 beta #status predicted <Mat>

Alignment Scores:
Pred. No.: 4,13e-05 Length: 266
Score: 131.50 Matches: 44
Percent Similarity: 45.68% Conservative: 30
Best Local Similarity: 27.16% Mismatches: 63
Query Match: 11.60% Indels: 25
Db: 1 Gaps: 8

```


US-09-869-566-4 (1-650) x S23010 (1-266)

```

QY      58 TACAAGAGATGACCAAGCT-----GGCGCCGCAATTCAGCTCTTTGAGA 108
Db      103 PheGluThrSerSeraspGluLeuCyaspAlaIalValGlnSerVallyCysLys 122
QY      109 GGTCCAAAGGTGAAGAACTTAAACCCGAAGAAATTCAGATTCAGCCAGATCAAA 168
Db      123 -----LeuGlnAspArgGluGlnLys 129
QY      169 GACTGCTCTGAGCTCTGGG-----AATTCATGACAGTTCAGATTAACATAC 219
Db      130 SerLeuValLeuAspSerProCysValLeuLysAlaLeuHisLeuProSerGlnGluMet 149
QY      220 ATACGCCAGAGATCTTTTTCATAGCCTCATCTGAGCTCAGCTCCTCGGAGAAA 279
Db      150 SerArg---GluValValPheCysMet---SerPheValGlnGlyGluLysAspAsn 167
QY      280 GGAAAGTCGATCTCTCGGGGGTCTCTAAAGGAGATTGTTGCTTACTGACAAAGAT 339
Db      168 LysIleProValAlaLeuGlyIleArgAspLysAsnLeuTyLeuSerCysValLys--- 186
QY      340 AAAGGCAAAAGTCATCCATCCCTTCAGCTGAGAGAGAACTGATGAAGCTGGCTGCC 399
Db      187 LysGlyAspThr---ProThrLeuGlnLeu-----GluGluValAspProLysValTy 203
QY      400 CAAAGGAATTCAGACAGCGCGCCCTCATCTTTATAGGGCTCAGGTGGGCTCTGGAAC 459
Db      204 ProLysArgAsnMetGluLysArgPheValPheTyLeuThrGluLeuLysAsnThrVal 223
QY      460 ATGCTGAGAGTCGCGGCTCACCCCGGATGATTCATGCACTTCGCAATTGTAAG 519
Db      224 GluPheGluSerValLeuTyProAsnTrpTyIleSerThrSerGlnIleGluGluLys 243
QY      520 CCTGTT 525
Db      244 ProVal 245

```

RESULT 9

JN0724
Interleukin-1 beta precursor - pig
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 14-Jul-1994 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: JN0724
R:Heuer, M.J.; Lin, G.; Smith, D.M.; Murtough, M.P.; Molitor, T.W.
Gene 129, 285-289, 1993
A:Title: Cloning, sequencing and regulation of an mRNA encoding porcine interleukin-1 beta
A:Reference number: JN0724; MUID:93314975; PMID:8325511
A:Accession: JN0724
A:Molecule type: mRNA
A:Residues: 1-267 <HEU>
A:Cross-references: UNIPROT:P26889; GB:M86725; NID:g164607; PIND:AAA02584.1; PID:g164608
A:Experimental source: alveolar macrophage
C:Comment: This protein is a pleiotropic cytokine that mediates a variety of processes in
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
ved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C:Superfamily: Interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag
F:115-267/Produce: interleukin-1 beta #status predicted <IL1>
F:77/Binding site: myristate (Lys) (covalent) #status predicted

Alignment Scores:

Pred. No.: 0.000442 Length: 267
Score: 121.50 Matches: 44
Percent Similarity: 42.35% Conservative: 28
Best Local Similarity: 25.88% Mismatches: 73
Query Match: 10.71% Indels: 25
DB: 1 Gaps: 7

US-09-869-566-4 (1-650) x JN0724 (1-267)

```

QY      64 GACGATGACGACAG-----CTTGGC 84
Db      86 AspAspArgGlnLysSerIlePheSerPheIlePheGluGluProIleIleLeuGlu 105
QY      85 GCCCGGAATTCAGCTCTTTGACAGAGTCCAAAGGTGAAGAACTTAAACCCGAAGAAATTC 144
Db      106 ThrCysAsnAspAspPheValCysAspAlaAsnValGlnSerMetGluCysLys----- 123
QY      145 AGCATTCATGACACAGATTCACAAAGTACTGCTCGAGTCTGGAGATCTCATACAGATT 204
Db      124 ---LeuGlnAspLysAspHisLysSerLeuValLeuAlaGlyProHisMetLeuLysAla 142
QY      205 CCAGAT-----AAATCATATACGCCAGAGATCTTTTTCATAGCTCATCTTGG 258
Db      143 LeuHisLeuLeuThrGlyAspLeuLysArgGluValAlaPheCysMet---SerPheVal 161
QY      259 ACCTACGCTCTGCGGAGAAAGAAAGTCCGATTCCTCGGGGTCTCTAAAGGAGATT 318
Db      162 GlnGlyAspAspSerAsnAsnLysIleProValThrLeuGlyIleLysGlyAsnLeu 181
QY      319 TGTCTTACTGT---GACAAAGATTAAGAGCAAAAGTCATCCCTTCAGCTGAAGAAG 375
Db      182 TyrLeuSerCysValMetLysAsp-----AsnThrProThrLeuGlnLeu----- 196
QY      376 GAGAAATGATGATAGCTGGCTGCCCAAAAGATCAGACGCGGCTTCATCTTTAT 435
Db      197 GluAspIleAspProLysArgTyrProLysArgAspMetGluLysArgPheValPheTy 216
QY      436 AGGGCTCAGGTGGCTCTCTCGAACAATGCTGAGTGGGGCTCACCCCGAGATGTTATC 495
Db      217 LysThrGlnIleLysAsnArgValGluPheGluSerAlaLeuTyProAsnTrpTyIle 236
QY      496 TGCACCTCTGCATTTGATGAGCCTGTT 525
Db      237 SerThrSerGlnAlaGluGlnLysProVal 246

```

RESULT 10

I55969
interleukin-1 beta precursor - mouse
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Mus musculus (house mouse)
C>Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: I55969; A24719; S13029
R:Gray, P.W.; Gaisler, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A:Title: Two interleukin-1 genes in the mouse: Cloning and expression of the cDNA for mu
A:Reference number: I55969; MUID:87058957; PMID:3491144
A:Accession: I55969
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-269 <RES>
A:Cross-references: UNIPROT:P10749; GB:M15131; NID:g198293; PIND:AAA39276.1; PID:g309398
R:Reiford, J.L.; Machuga, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9925-9963, 1986
A:Title: The murine interleukin-1-beta gene: structure and evolution.
A:Reference number: A24719; MUID:87117546; PMID:3492706
A:Accession: A24719
A:Molecule type: mRNA
A:Residues: 1-269 <TEL>
A:Cross-references: GB:X04964; NID:g52666; PIND:CAA28637.1; PID:g52667
R:Daumy, G.O.; Wilder, C.B.; Merenda, J.M.; McColi, A.S.; Geoghegan, K.F.; Otterness, I.C
FEBS Lett. 278, 98-102, 1991
A:Title: Reduction of biological activity of murine recombinant interleukin-1beta by sele
A:Reference number: S13029; MUID:91130610; PMID:1993481
A:Accession: S13029
A:Status: preliminary
A:Molecule type: protein
A:Residues: 118-269 <DAU>
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
ved form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C:Gene: IL-1-beta

C:Superfamily: interleukin-1

C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F:118-269/Product: interleukin-1 beta #status experimental <IL1>

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score:	0.000561	269	120.50	50	34
Percent Similarity:	46.67%				
Best Local Similarity:	27.78%				
Query Match:	10.63%				
DB:	1	Gaps:	9		

US-09-869-566-4 (1-650) x I55969 (1-269)

```

QY 49 GTTGCTGATACAAAGCATGACGAAAGCTTGCGCGCAATTCAGCTCTTGACGA 108
DB 103 LeuCyAspSerTrpAspAspAsp-----AsnLeuValCysAsp 117
QY 109 GGTCCAAAGGTGAAGAACTTAAACCCGAAGAAATTCAGATCAGCAGATCAAA 168
DB 118 ValPro---IleArgIleuHis-----TyrArgLeuArgAspGluGlnGln 133
QY 169 GATCTGCTCTG---GACTCTGGGAATCTCATAGCAGTTCA---GATAAACTACATA 222
DB 134 SerLeuValIleuSerAspProTyrGluLeuValAlaLeuHisIleuAsnGlnGlnAsnIle 153
QY 223 CCGCCAGAAATCTTCTTGATGATGACCTTGAAGCTCAGCTCTGCGAAGAAAGA 282
DB 154 AsnGlnGlnValIleHisSerMetSerPheValGlnGlnGluProSerAsnAspLys--- 172
QY 283 AGTCCGATCTCTCGGGGGCTCTCTAAAGGGAAGTTTGTCTACCTGATGACAAAGATAA 342
DB 173 IleProValAlaLeuGlnIleuLysGlnLysAsnLeuTyrLeuSerCysValMetLysAsp 192
QY 343 GGACAAAGTCAATTCATCCCTTCACTGAGTGAAGAAAGAACTGAAGAGCTGCGCCAA 402
DB 193 GlyThr-----ProThrIleuGlnLeu-----GluSerValAspProLysGlnTyrPro 208
QY 403 AAGGAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATG 462
DB 209 LysLysValMetGlnLysArgPheValPheAsnLysIleGluValLysSerLysValGlu 228
QY 463 CTGAGAGTCGGCGGCTCAGCCCGGATTCATCTGACCTGCAATTTGATATGAGCT 522
DB 229 PheGluSerAlaGluPheProAsnTyrIleSerThrSerGlnAlaGluHisLysPro 248
QY 523 GTTGGGTGACAGATTAATTTGAGAACAGAAACACATTGAATTTTCATTCCACCACT 582
DB 249 ValPheLeuGlnYAsnAsn---SerGlnGlnAspIleIleAspPheThrMetGluSerVal 267

```

RESULT 11

ICB01B

Interleukin-1 beta precursor - bovine

N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: J10010; S01380

R:Mailiszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gillis, S.; Mol. Immunol. 25, 429-437, 1988

A:Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleukin

A:Reference number: A9695; MUID:88318652; PMID:3261832

A:Accession: J10010

A:Molecule type: mRNA

A:Residues: 1-266 <MAL>

A:Cross-references: UNIPROT:P09428; GB:M37211; NID:g163200; PIDD:AAA30584.1; PID:g163201

R:Leong, S.R.; Flagers, G.M.; Lammann, M.; Gray, P.W. Nucleic Acids Res. 16, 9054, 1988

A:Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.

A:Reference number: S01380; MUID:89016591; PMID:3262866

A:Accession: S01380

A:Molecule type: mRNA

A:Residues: 1-251/'A', 253-266 <LEO>

A:Cross-references: EMBL:X12498; NID:g448; PIDD:CAA31018.1; PID:g449

C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and involved form of interleukin-beta, unlike interleukin 1-alpha, is inactive.

C:Superfamily: interleukin-1

C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen

F:114-266/Product: interleukin-1 beta #status predicted <MAT>

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:
Score:	0.00101	266	118.00	46	33
Percent Similarity:	43.65%				
Best Local Similarity:	25.41%				
Query Match:	10.41%				
DB:	1	Gaps:	8		

US-09-869-566-4 (1-650) x ICB01B (1-266)

```

QY 34 CTGTTGAGCTGAGCTGCTGATCAAAAGCATGACGAAAGCTTGC----- 84
DB 74 LeuArgAsnSerIleTyrAlaHisValPheHisAspAspAspLeuArgSerIleuSer 93
QY 85 -----GCCGCAATTCAGCTCTTGACGA 108
DB 94 PheIlePheGluGluGluProValIlePheGluThrSerSerAspGluPheLeuCysAsp 113
QY 109 GGTCCAAAGGTGAAGAACTTAAACCCGAAGAAATTCAGATCAGCAGATCAAA 168
DB 114 AlaPro---ValGlnSerIle-----LysCysLysLeuGlnAspArgGlnGlnLys 129
QY 169 GATCTGCTCTGAGCTCTGGAATCTCATAGCAGATTCAGAT-----AAAACTACATA 222
DB 130 SerLeuValIleuAlaSerProCysValIleuLysAlaLeuHisIleuLeuSerGlnGlnMet 149
QY 223 CCGCCAGAAATCTTCTTGATGATGACCTTGAAGCTCAGCTCTGCGAAGAAAGA 282
DB 150 AsnArgGluValIleValPheCysMet---SerPheValGlnGlnGluLysArgAsnLys 168
QY 283 AGTCCGATCTCTCGGGGCTCTCTAAAGGGAAGTTTGTCTACCTGATGACAAAGATAA 342
DB 169 IleProValAlaLeuGlnIleLysAspLysAsnLeuTyrLeuSerCysValLys--Lys 187
QY 343 GGACAAAGTCAATTCATCCCTTCACTGAGTGAAGAAAGAACTGAAGAGCTGCGCCAA 402
DB 188 GlyAspThr---ProThrIleuGlnLeu-----GluGluValAspProLysValTyrPro 204
QY 403 AAGGAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATG 462
DB 205 LysValGlnMetGlnLysArgPheValPheTyrLysThrGlnIleLysAsnThrValGlu 224
QY 463 CTGAGAGTCGGCGGCTCAGCCCGGATTCATCTGACCTGCAATTTGATATGAGCT 522
DB 225 PheGluSerValLeuTyrProAsnTyrIleSerThrSerGlnIleGluGluArgPro 244
QY 523 GTT 525
DB 245 Val 245

```

RESULT 12

ICB01B

Interleukin-1 beta precursor [validated] - human

N:Alternate names: hematopoietin-1; IL-1 beta

C:Species: Homo sapiens (man)

C>Date: 28-Feb-1986 #sequence revision 15-May-1998 #text_change 09-Jul-2004

C:Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848; S196

R:Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E. Nucleic Acids Res. 14, 7897-7914, 1986

A:Title: Genomic sequence for human interleukin 1 beta: possible evolution from a rev

A:Reference number: A25542; MUID:87040762; PMID:3490654

A:Accession: A25542

A:Molecule type: DNA; mRNA

A:Residues: 1-5/'K', 7-269 <CLA>

A:Cross-references: UNIPROT:P01584; GB:X04500; NID:g33788

A>Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Glu
 A:Beni, G.; Rangel, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Meili, M.
 Gene 52, 95-101, 1987
 A:Title: Human interleukin-1 beta gene
 A:Reference number: A29019; MUID:87248099; PMID:2954882
 A:Accession: A29019
 A:Molecule type: DNA
 A:Residues: 1-269 <BEN>
 A:Cross-references: GB:M15840; NID:9186281; PIDN:AAA74137.1; PID:9386816
 R:Auron, P.E.; Webb, A.C.; Rosemasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Dinare
 Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
 A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
 A:Reference number: A94023; MUID:85088517; PMID:6083565
 A:Accession: A94023
 A:Molecule type: mRNA
 A:Residues: 1-5, 'K', 7-269 <AUR>
 A:Cross-references: GB:K02770; NID:9186268; PIDN:AAA6106.1; PID:9307043
 R:March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis, S.
 Nature 315, 641-647, 1985
 A:Title: Cloning, sequence and expression of two distinct human interleukin-1 complement
 A:Reference number: A93361; MUID:85240547; PMID:2989698
 A:Accession: A93361
 A:Molecule type: mRNA
 A:Residues: 1-269 <MAR>
 A:Cross-references: GB:X02532; NID:933789; PIDN:CAA26372.1; PID:933790
 A>Note: parts of this sequence, including the amino end of the mature form, were confirm
 R:Webb, A.C.; Dinarello, C.A.; Rosemasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Au
 Adv. Gene Technol. 22, 339-340, 1985
 A:Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
 A:Reference number: 151852
 A:Accession: 151852
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEB>
 A:Cross-references: GB:M54933; NID:9186287; PIDN:AAA59136.1; PID:9186288
 R:Nishida, T.; Nishino, N.; Takano, K.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; Hirai
 Biochem. Biophys. Res. Commun. 143, 345-352, 1987
 A:Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
 A:Reference number: 152217; MUID:87156769; PMID:3493774
 A:Accession: 152217
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-269 <NIS>
 A:Cross-references: GB:M15330; NID:9186283; PIDN:AAA59135.1; PID:9307045
 R:Kotenko, S.V.; Bulenkov, M.T.; Velko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov,
 I.I.; S.A.; Vinetkili, Y.P.
 Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
 A:Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin
 A:Reference number: 138131; MUID:90249285; PMID:2635664
 A:Accession: 138132
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-269 <ROT>
 A:Cross-references: EMBL:X56087; NID:935662; PIDN:CAA39567.1; PID:935663
 R:Sebo, K.M.; Wypych, J.; Yusechenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.
 Blood 71, 962-966, 1988
 A:Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic
 A:Reference number: A90732; MUID:88184226; PMID:3281727
 A:Accession: B27616
 A:Molecule type: protein
 A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSB>
 R:Stevenson, F.T.; Burenson, S.L.; Fantom, C.; Locksley, R.M.; Lovett, D.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
 A:Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines
 A:Reference number: A48293; MUID:93348250; PMID:8346241
 A:Contents: annotation; myristylation of lysines
 R:Handuri, V.B.; Hughes, J.D.; Pan, Y.C.; Kilian, P.L.; Stern, A.S.
 Biochem. Biophys. Acta 1118, 25-35, 1991
 A:Title: The role of arginine residues in interleukin 1 receptor binding.
 A:Reference number: S19608; MUID:92110334; PMID:1837236
 A:Contents: annotation; type 1 IL-1 receptor interaction site
 A>Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
 R:Clore, G.M.; Gronenborn, A.M.

submitted to the Brookhaven Protein Data Bank, January 1991
 A:Reference number: A50049; PDB:611B
 A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
 R:Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
 Biochemistry 30, 2315-2323, 1991
 A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution by
 A:Reference number: A44675; MUID:91159409; PMID:2001363
 A:Contents: annotation; (1)H-NMR structural determination
 R:Hazda, D.J.; Strickler, J.; Simon, P.; Young, P.R.
 J. Biol. Chem. 266, 7081-7086, 1991
 A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a conf
 A:Reference number: A39774; MUID:91201363; PMID:2016316
 A:Contents: annotation
 R:Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
 submitted to the Brookhaven Protein Data Bank, December 1989
 A:Reference number: A50016; PDB:111B
 R:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspahr,
 J. Mol. Biol. 209, 779-791, 1989
 A:Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolut
 A:Reference number: A44666; MUID:90064532; PMID:2585509
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a)
 C:Genes: GDB:IL1B
 A:Cross-references: GDB:120094; OMIM:147720
 A:Map position: 2q13-2q21
 A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage
 F:117-269/Product: interleukin-1 beta status experimental <IL1>
 F:6/Binding site: myristate (Lys) (covalent) (partial) #status experimental
 F:23/Binding site: carbohydrate (Asn) (covalent) #status absent

Alignment Scores:

	Pred. No.:	Length:	Matches:	Mismatches:
Score:	0.116	269	98.00	42
Best Local Similarity:	46.00%		Conservative:	27
Query Match:	8.64%		Indels:	16
DB:	1	Gaps:	8	

US-09-869-566-4 (1-650) x ICHU1B (1-269)

```

QY  91 AATTGAGCTCTTTCGACGAGCTCCAAAGCTTAACCCGAAGAATTACGACATT 150
    |||||
DB  110 AaagguhlatytrValHisaplaaproValArgserLeuasn-----Cysthrleu 126

QY  151 CATGACGAGATCACAAGATCTGGCTCGACTCGG-----AATCTCATGACGATT 204
    |||||
DB  127 Argaspserserglnlyserleuvalmet---serglyProtygluleuylsalaen 145

QY  205 CCAGATMAAAACTAC---ATACGCCAGAGATCTTTTGATTAAGCTCATCTTGAGC 261
    |||||
DB  146 HsleuGlnGlyGlaaspmetGluGlnGlnValalPheSerMeeserPheValGlnGly 165

QY  262 TCAAGCTCTCGCGAAGAAAGAGTCCGATTCCTCGGGGCTCTTAAGGAGATTTCCT 321
    |||||
DB  166 GluGlnSerAsnAspLys---lleProValAlaaleGlyLeuylsleuylsbenLeuTyR 184

QY  322 CTCTACTGT-----GACAAGATTAAGCAAAAGTCATCCATCCCTTCAGCTGAAGAAG 375
    |||||
DB  185 leuSerCysValleuylsAspLys-----ProthrleuGln----- 198

QY  376 GAGAACTGATGAAAGCTGCTGCCCAAAAGATCAGACGCGGCTTCATCTTTTAT 435
    |||||
DB  199 GluSerValAspProlysasnTyrrProylsLysLysMetGluLysArgPheValPheasn 218

QY  436 AGGGCTCAGGTGGGCTCTCGAATCATGCTGAGTGGGGCTCACCCCGGATGCTTCATC 495
    |||||
DB  219 LyslleGlnlleAsnAsnLysleuGlnPheGlnSerAlaGlnPheProasnTrpTyrlle 238
  
```


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OM nucleic - protein search, using frame_plus.n2p model

Run on: May 28, 2005, 17:32:11 ; Search time 72 seconds
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Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USRR=US09869566 @CGN_1.1.130 @runat_27052005_163131_19970
-NCPu=6 -ICPU=3 -NO_MMAP -LARGEJURY -NEG_SCORES=0 -WAIT -DSPELCHK=100
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	906	79.9	192	10	US-09-876-790-3	Sequence 3, Appli
2	906	79.9	192	14	US-10-139-833-13	Sequence 13, Appli
3	906	79.9	192	17	US-10-888-779-3	Sequence 3, Appli
4	906	79.9	192	17	US-10-888-867-3	Sequence 3, Appli
5	906	79.9	192	17	US-10-888-780-3	Sequence 3, Appli
6	906	79.9	192	17	US-10-888-911-3	Sequence 3, Appli
7	902	79.5	197	10	US-09-876-790-9	Sequence 9, Appli
8	902	79.5	197	17	US-10-888-779-9	Sequence 9, Appli
9	902	79.5	197	17	US-10-888-867-9	Sequence 9, Appli
10	902	79.5	197	17	US-10-888-780-9	Sequence 9, Appli
11	902	79.5	197	17	US-10-888-931-9	Sequence 9, Appli
12	895	78.9	198	9	US-09-788-963-6	Sequence 6, Appli
13	895	78.9	218	9	US-09-788-963-2	Sequence 2, Appli
14	895	78.9	218	10	US-09-876-790-8	Sequence 8, Appli
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16	895	78.9	218	14	US-10-302-554-2	Sequence 2, Appli
17	895	78.9	218	15	US-10-695-195-4	Sequence 4, Appli
18	895	78.9	218	15	US-10-694-978-4	Sequence 4, Appli
19	895	78.9	218	15	US-10-679-201-6	Sequence 6, Appli
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ALIGNMENTS

US-09-876-790-3
; Sequence 3, Application US/09876790
; Publication No. US20030091532A1
GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTID
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 192

TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-790-3

Alignment Scores:

Pred. No.:	2,51e-91	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	10	Gaps:	0

US-09-869-566-4 (1-650) x US-09-876-790-3 (1-192)

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QY 166 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAGTTCCAGATTAATACTACATACGC 225
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DB 42 LysValLeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrlleArg 61
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DB 62 ProGluIlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLysGlySer 81
QY 286 CCGATTCTCTGGGGGCTCTTAAAGGGAGATTCTTCTACTGTGACAAAGATAAGGA 345
    |||||
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RESULT 2

US-10-139-833-13

Sequence 13, Application US/10139833

Publication No. US20030004106A1

GENERAL INFORMATION:

APPLICANT: Sartis, Christiaan M.

APPLICANT: Giles, Jennifer

APPLICANT: Mu, Sharon X.

APPLICANT: Xia, Min

APPLICANT: Babs, Michael B.

APPLICANT: Craveiro, Roger

TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and

FILE REFERENCE: 00-1213-E

CURRENT APPLICATION NUMBER: US/10/139,833

PRIOR FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: 60/170,191

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: 60/188,053

PRIOR FILING DATE: 2000-03-09

PRIOR APPLICATION NUMBER: 60/194,521

PRIOR FILING DATE: 2000-04-04

PRIOR APPLICATION NUMBER: 60/195,910

PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 09/724,583
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13

LENGTH: 192

TYPE: PRT

ORGANISM: Homo sapiens

US-10-139-833-13

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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	14	Gaps:	0

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RESULT 3

US-10-888-779-3

Sequence 3, Application US/10888779

Publication No. US20050009138A1

GENERAL INFORMATION:

APPLICANT: SIMS, John E.

APPLICANT: Smith, Dick E.

APPLICANT: BORN, Teresa L.

TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRECE DNAS AND POLYPEPTII

FILE REFERENCE: 2008-US

CURRENT APPLICATION NUMBER: US/10/888,779

PRIOR FILING DATE: 2004-07-09

PRIOR APPLICATION NUMBER: US/09/876,790

PRIOR FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: 60/112,163

PRIOR FILING DATE: 1998-12-14

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; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-779-3

Alignment Scores:
Pred. No.: 2,51e-91 Length: 192
Score: 906.00 Matches: 171
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.89% Indels: 0
DB: 17 Gaps: 0

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RESULT 4
US-10-888-867-3
; Sequence 3, Application US/1088867
; Publication No. US2005009075A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,867
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
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; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-867-3

Alignment Scores:
Pred. No.: 2,51e-91 Length: 192
Score: 906.00 Matches: 171
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 79.89% Indels: 0
DB: 17 Gaps: 0

US-09-869-566-4 (1-650) x US-10-888-867-3 (1-192)

QY 106 AAGGTCGCAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACGAGATCAC 165
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QY 166 AAGTACTGCTGCTGAGCTCTGGGAATCTCATGACATTCAGATTAATAAATCAATACGC 225
DB 42 LysValIleuValIleuAspSerGlyAsnLeuIlleAlaValProAspLysAsnTyrlleArg 61
QY 226 CCAGAGATCTTCTTGATTAAGCTCATCTGAGCTCAGCTGCGGAGAAAGAGAT 285
DB 62 ProGluIlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIlleGlnlySer 81
QY 286 CCGATTCTCTGCGGCTCTCTAAAGGAGATTGTCTCTACTGTGACAGATAAAGA 345
DB 82 ProIleuLeuGlyValSerIySgIyGluPheCySleuTyCyAspLysAspLysGly 101
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QY 406 GAATGACAGACGCGGCTTCATCTTTATAGGCTCAGAGTGGGCTCCTGAACATGCTG 465
DB 122 GlnSerAlaArgArgProPheIlePheTyrlArgAlaGlnValGlySerTrpAsnMetLeu 141
QY 466 GAGTCGCGGCTCACCCGAGATGTTTCATCTGACCTCCTGCAATTGTAATGAGCTGTT 525
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DB 162 GlyValIThrAspLysPheGlnAsnArgLysHisIleGlnPheSerPheGlnProValCys 181
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DB 182 LysAlaGlnMetSerProSerGlnValSerAsp 192

RESULT 5
US-10-888-780-3
; Sequence 3, Application US/10888780
; Publication No. US20050013797A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,780
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
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;; PRIOR APPLICATION NUMBER: 60/112,163
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: 60/146,675
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: PCT/US99/29549
;; PRIOR FILING DATE: 1999-12-14
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-10-888-780-3

Alignment Scores:

Pred. No.:	2,51e-91	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	17	Gaps:	0

US-09-869-566-4 (1-650) x US-10-888-780-3 (1-192)

QY 106 AAGGTCCTCAAGGTGAGAACTTAAACCGAAGAAATTCAGATTTCATGACGAGATCAC 165
DB 22 ArgGlyProIyValIyAsnLeuAnProIyLysPheSerIleHisAspGlnAspHis 41
QY 166 AAGTACTGTGCTCTGAGCTCTGGGAATCTCATAGCAATTCAGATTAATAAATCACTAAGC 225
DB 42 LysValIleValIleuAspSerGlyAsnLeuIleAlaValProAspLysAsnIyrlIeArg 61
QY 226 CCAGAGATCTTCTTGATGATGAGCTTCATGAGCTTCAGCTTCGCGAAGAAAGAGT 285
DB 62 ProGluIlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleGluIySer 81
QY 286 CCGATTCTCTGGGGGTCTTAAAGGAGATTGTCTCTACTGTGACAAGATAAGAA 345
DB 82 ProIleLeuIleGlyValIleSerIyGlyIuPheCysLeuIyrcYAspLysAspIySgly 101
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DB 102 GlnSerHisProSerLeuGlnLeuIyLysGlyLysLeuMetCysLeuAlaIleGlnLys 121
QY 406 GAATCAGACGCGCGGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 465
DB 122 GluSerAlaIleArgArgProPheIlePheIyTrArgAlaGlnValGlySerTrpAsnMetLeu 141
QY 466 GAGTCGGGGCTCACCCCGAGATGTTTCATCTGACCTCTCGCAATTGTATAGAGCTGTT 525
DB 142 GluSerAlaIleAlaHisProGlyTrpPheIleCysThrSerCysAsnCysAsnGlnProVal 161
QY 526 GGGGTGACAGATTAATTGAGAACAGAAACACATTTGATTTTCATTCAACCATTTGCG 585
DB 162 GlyValIleThrAspLysPheGlnuAsnArgLysHisIleGluPheSerPheGlnProValCys 181
QY 586 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCAT 618
DB 182 LysAlaGluMetSerProSerGlnuValSerAsp 192

RESULT 6

US-10-888-931-3
;; Sequence 3, Application US/10888931
;; Publication No. US20050013798A1
;; GENERAL INFORMATION:
;; APPLICANT: SIMS, John E.
;; APPLICANT: SMITH, Dirk E.
;; APPLICANT: BORN, Teresa L.
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI
;; FILE REFERENCE: 2008-US
;; CURRENT APPLICATION NUMBER: US/10/888,931
;; CURRENT FILING DATE: 2004-07-09
;; PRIOR APPLICATION NUMBER: US/09/876,790

;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: 60/112,163
;; PRIOR FILING DATE: 1998-12-14
;; PRIOR APPLICATION NUMBER: 60/146,675
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: PCT/US99/29549
;; PRIOR FILING DATE: 1999-12-14
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 3
;; LENGTH: 192
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-10-888-931-3

Alignment Scores:

Pred. No.:	2,51e-91	Length:	192
Score:	906.00	Matches:	171
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	79.89%	Indels:	0
DB:	17	Gaps:	0

US-09-869-566-4 (1-650) x US-10-888-931-3 (1-192)

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DB 22 ArgGlyProIyValIyAsnLeuAnProIyLysPheSerIleHisAspGlnAspHis 41
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DB 42 LysValIleValIleuAspSerGlyAsnLeuIleAlaValProAspLysAsnIyrlIeArg 61
QY 226 CCAGAGATCTTCTTGATGATGAGCTTCATGAGCTTCAGCTTCGCGAAGAAAGAGT 285
DB 62 ProGluIlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerIleGluIySer 81
QY 286 CCGATTCTCTGGGGGTCTTAAAGGAGATTGTCTCTACTGTGACAAGATAAGAA 345
DB 82 ProIleLeuIleGlyValIleSerIyGlyIuPheCysLeuIyrcYAspLysAspIySgly 101
QY 346 CAAAGTCATCCATCCCTTCAGCTGAGAGAGAACTGATGAAGCTGGCTGCCCAAG 405
DB 102 GlnSerHisProSerLeuGlnLeuIyLysGlyLysLeuMetCysLeuAlaIleGlnLys 121
QY 406 GAATCAGACGCGCGGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 465
DB 122 GluSerAlaIleArgArgProPheIlePheIyTrArgAlaGlnValGlySerTrpAsnMetLeu 141
QY 466 GAGTCGGGGCTCACCCCGAGATGTTTCATCTGACCTCTCGCAATTGTATAGAGCTGTT 525
DB 142 GluSerAlaIleAlaHisProGlyTrpPheIleCysThrSerCysAsnCysAsnGlnProVal 161
QY 526 GGGGTGACAGATTAATTGAGAACAGAAACACATTTGATTTTCATTCAACCATTTGCG 585
DB 162 GlyValIleThrAspLysPheGlnuAsnArgLysHisIleGluPheSerPheGlnProValCys 181
QY 586 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCAT 618
DB 182 LysAlaGluMetSerProSerGlnuValSerAsp 192

RESULT 7

US-09-876-790-9
;; Sequence 9, Application US/09876790
;; Publication No. US20030091532A1
;; GENERAL INFORMATION:
;; APPLICANT: SIMS, John E.
;; APPLICANT: SMITH, Dirk E.
;; APPLICANT: BORN, Teresa L.
;; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI
;; FILE REFERENCE: 2008-US
;; CURRENT APPLICATION NUMBER: US/09/876,790
;; CURRENT FILING DATE: 2002-09-04

; PRIOR APPLICATION NUMBER: 60/112,163
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: 60/146,675
 ; PRIOR FILING DATE: 1999-11-10
 ; PRIOR APPLICATION NUMBER: PCT/US99/29549
 ; PRIOR FILING DATE: 1999-12-14
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-876-790-9

Alignment Scores:

Pred. No.:	7	04e-91	Length:	197
Score:	902.00	Matched:	172	
Percent Similarity:	93.62%	Conservative:	4	
Best Local Similarity:	91.49%	Mismatches:	6	
Query Match:	79.54%	Indels:	6	
DB:	10	Gaps:	1	

US-09-869-566-4 (1-650) x US-09-876-790-9 (1-197)

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QY 55 GACTACAAAGAGATGACGACGAGCTTGGCGGCGGAAATTCAGCTCTTTGACAGAGTCCA 114
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DB 16 AAPTTPGLULYASPGILUPROGIN-----CyeCylseuGluglYPro 29
QY 115 AAGGTGAAGAACTTAAACCCGAAAGAAATTCAGATTCATGACGAGATCAAAAGTACTG 174
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 30 LysValIyAsnLeuAsnProIySlySpheSerIleHIsAspGlnAspHisIySValIeu 49
QY 175 GTCTGGAAGCTCTGGGAATCTATAGACAGTCCAGATTAATACTACATAGCCGACAGATC 234
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 50 ValIeuAspSerGlyAsnLeuIleAlaValProAspLysAsnIyrlIeArProGluIle 69
QY 235 TTCTTTGATTAGCCTCATCTTGAAGCTCAGCCTCTGCGGAGAAAGAAATTCGATTC 294
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 70 PhePheAlaLeuAlaSerSerIeuSerSerAlaSerAlaGluIySglYserProIleIeu 89
QY 235 CTGGGGGCTCTTAAGGGAGATTGTTGCTCTACTGTGACAGATTAAGAGCAAAATCAT 354
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 90 LeuGlyValSerIySglYlupheCySleuIyrcySAspLysAspLysGlyIserHis 109
QY 355 CCATCCCTTCAGCTGTAAGAGAGAACTGATGAAGCTGGCTGCCAAAGAAATTCAGCA 414
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 110 ProSerLeuGlnLeuIySglYlupheCylsleuIyrcySAspLysAspLysGlyIserHis 129
QY 415 CGCCGGGCTTCATCTTTATAGGCTCAGGTGAGGCTCCTGGAACATGCTGAGTGGCG 474
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 130 ArgArgProPheIlePheIytrArgAlaGlnValGlySerTrpAsnMetLeuGlnSerAla 149
QY 475 GCTCAACCCCGATGGTTCACTGACCTCTCGCAATTTGAATGAGCTGTGGGGTGACA 534
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 150 AlaHisProGlyIyTrpPheIleCySerHisrcySAsnGlnProValGlyAlaThr 169
QY 535 GATTAATTGGAAGAAGAAACATGAAATTTTCAACCGAGTTGCAAGTGA 594
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 170 AspLysPheGlnAsnArgLysHisIleGluPheSerPheGlnProValCylsValaGlu 189
QY 595 ATGAGCCCGAGTGAAGTCAAGCAT 618
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DB 190 MetSerProSerGlnValSerAsp 197
  
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RESULT 8

US-10-888-779-9
 ; Sequence 9, Application US/10888779
 ; Publication No. US20050009138A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMS, John E.
 ; APPLICANT: SMITH, Dirk E.
 ; APPLICANT: BORN, Teresa L.
 ; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI

; FILE REFERENCE: 2008-US
 ; CURRENT APPLICATION NUMBER: US/10/888,779
 ; CURRENT FILING DATE: 2004-07-09
 ; PRIOR APPLICATION NUMBER: US/09/876,790
 ; PRIOR FILING DATE: 2001-06-06
 ; PRIOR APPLICATION NUMBER: 60/112,163
 ; PRIOR FILING DATE: 1998-12-14
 ; PRIOR APPLICATION NUMBER: 60/146,675
 ; PRIOR FILING DATE: 1999-11-10
 ; PRIOR APPLICATION NUMBER: PCT/US99/29549
 ; PRIOR FILING DATE: 1999-12-14
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 197
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-888-779-9

Alignment Scores:

Pred. No.:	7	04e-91	Length:	197
Score:	902.00	Matched:	172	
Percent Similarity:	93.62%	Conservative:	4	
Best Local Similarity:	91.49%	Mismatches:	6	
Query Match:	79.54%	Indels:	6	
DB:	17	Gaps:	1	

US-09-869-566-4 (1-650) x US-10-888-779-9 (1-197)

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QY 55 GACTACAAAGAGATGACGACGAGCTTGGCGGCGGAAATTCAGCTCTTTGACAGAGTCCA 114
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DB 16 AAPTTPGLULYASPGILUPROGIN-----CyeCylseuGluglYPro 29
QY 115 AAGGTGAAGAACTTAAACCCGAAAGAAATTCAGATTCATGACGAGATCAAAAGTACTG 174
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 30 LysValIyAsnLeuAsnProIySlySpheSerIleHIsAspGlnAspHisIySValIeu 49
QY 175 GTCTGGAAGCTCTGGGAATCTATAGACAGTCCAGATTAATACTACATAGCCGACAGATC 234
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 50 ValIeuAspSerGlyAsnLeuIleAlaValProAspLysAsnIyrlIeArProGluIle 69
QY 235 TTCTTTGATTAGCCTCATCTTGAAGCTCAGCCTCTGCGGAGAAAGAAATTCGATTC 294
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DB 70 PhePheAlaLeuAlaSerSerIeuSerSerAlaSerAlaGluIySglYserProIleIeu 89
QY 235 CTGGGGGCTCTTAAGGGAGATTGTTGCTCTACTGTGACAGATTAAGAGCAAAATCAT 354
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 90 LeuGlyValSerIySglYlupheCySleuIyrcySAspLysAspLysGlyIserHis 109
QY 355 CCATCCCTTCAGCTGTAAGAGAGAACTGATGAAGCTGGCTGCCAAAGAAATTCAGCA 414
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 110 ProSerLeuGlnLeuIySglYlupheCylsleuIyrcySAspLysAspLysGlyIserHis 129
QY 415 CGCCGGGCTTCATCTTTATAGGCTCAGGTGAGGCTCCTGGAACATGCTGAGTGGCG 474
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 130 ArgArgProPheIlePheIytrArgAlaGlnValGlySerTrpAsnMetLeuGlnSerAla 149
QY 475 GCTCAACCCCGATGGTTCACTGACCTCTCGCAATTTGAATGAGCTGTGGGGTGACA 534
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 150 AlaHisProGlyIyTrpPheIleCySerHisrcySAsnGlnProValGlyAlaThr 169
QY 535 GATTAATTGGAAGAAGAAACATGAAATTTTCAACCGAGTTGCAAGTGA 594
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 170 AspLysPheGlnAsnArgLysHisIleGluPheSerPheGlnProValCylsValaGlu 189
QY 595 ATGAGCCCGAGTGAAGTCAAGCAT 618
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DB 190 MetSerProSerGlnValSerAsp 197
  
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RESULT 9

US-10-888-867-9
 ; Sequence 9, Application US/1088867
 ; Publication No. US20050009075A1

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/ GENERAL INFORMATION:
/ APPLICANT: SIMS, John E.
/ APPLICANT: SMITH, Dirk E.
/ APPLICANT: BORN, Teresa L.
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI
/ FILE REFERENCE: 2008-US
/ CURRENT APPLICATION NUMBER: US/10/888,867
/ PRIOR FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: US/09/876,790
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/112,163
/ PRIOR FILING DATE: 1998-12-14
/ PRIOR APPLICATION NUMBER: 60/146,675
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: PCT/US99/29549
/ PRIOR FILING DATE: 1999-12-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 197
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-888-867-9

Alignment Scores:
Pred. No.: 7.04e-91 Length: 197
Score: 902.00 Matches: 172
Percent Similarity: 93.62% Conservative: 4
Best Local Similarity: 91.49% Mismatches: 6
Query Match: 79.54% Indels: 6
DB: 17 Gaps: 1

US-09-869-566-4 (1-650) x US-10-888-867-9 (1-197)
QY 55 GACTAACAAGACGATGACGACAAAGCTGGCGCGCAATTGACGCTTTGGAGAGTCCA 114
Db 16 AaPTpGluLyAspGluProGln-----CysCysLeuGluGlyPro 29
QY 115 AAGGTGAAGAAGCTTAAACCCGAAGAAATTCAGCATTCATGACCAAGATGCTG 174
Db 30 LySVaLlyAsnLeuAsnProLySlySpheSerLleHisAspGlnAspHislySVaLleu 49
QY 175 GTCTCGAGCTCTGGGAATTCATAGCAGTTCCAGATTAATAACTACATACGCCAGATC 234
Db 50 ValLeuAspSerGlyAsnLeuLeaValProAspLyAsnTyrlleArgProGluIle 69
QY 235 TTTCTTGCAATGACCTTCATCCTTGAGCTCAGCCTCGCGAAGAAAGAAAGTTC 294
Db 70 PhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLySglYserProIleLeu 89
QY 295 CTGGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGCAAGTCA 354
Db 90 LeuGlyValSerlySglYgluPheCysLeuTyrcyAspLyAspLySglYgluInserrHis 109
QY 355 CCATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTGGCTGCCAAAAGAAATCAGA 414
Db 110 ProSerLeuGlnLeuLySglYgluPheCysLeuTyrcyAspLyAspLySglYgluInserrHis 129
QY 415 CGCGGCGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTCTGAAACATGCTGAGTGGGG 474
Db 130 ArgArgProPheLlePheTyArgAlaGlnValGlySerTyrPasmheCysLeuGlnSerAla 149
QY 475 GCTCAACCCGAGATGTTCACTGACCTCTGCAATTGATGAGCTGTGGGGTGA 534
Db 150 AlaHisProGlyTyrPheLleCysThrSerCysAsnCyAsnGlnProValGlyValThr 169
QY 535 GATTAATTTGAGAACAGAAACACATGATTTTCAACCAAGTTCGAAAGCTGAA 594
Db 170 AspLyPheGluAsnArgLySHisLleGluPheSerPheGlnProValCysLySAlaGlu 189
QY 595 ATGAGCCCAAGTAGGCTCAGCCAT 618
Db 190 MetSerProSerGlnValSerAsp 197
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RESULT 10
US-10-888-780-9
/ Sequence 9, Application US/10888780
/ Publication No. US20050013797A1
/ GENERAL INFORMATION:
/ APPLICANT: SIMS, John E.
/ APPLICANT: SMITH, Dirk E.
/ APPLICANT: BORN, Teresa L.
/ TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTII
/ FILE REFERENCE: 2008-US
/ CURRENT APPLICATION NUMBER: US/10/888,780
/ PRIOR FILING DATE: 2004-07-09
/ PRIOR APPLICATION NUMBER: US/09/876,790
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/112,163
/ PRIOR FILING DATE: 1998-12-14
/ PRIOR APPLICATION NUMBER: 60/146,675
/ PRIOR FILING DATE: 1999-11-10
/ PRIOR APPLICATION NUMBER: PCT/US99/29549
/ PRIOR FILING DATE: 1999-12-14
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 9
/ LENGTH: 197
/ TYPE: PR
/ ORGANISM: Homo sapiens
US-10-888-780-9

Alignment Scores:
Pred. No.: 7.04e-91 Length: 197
Score: 902.00 Matches: 172
Percent Similarity: 93.62% Conservative: 4
Best Local Similarity: 91.49% Mismatches: 6
Query Match: 79.54% Indels: 6
DB: 17 Gaps: 1

US-09-869-566-4 (1-650) x US-10-888-780-9 (1-197)
QY 55 GACTAACAAGACGATGACGACAAAGCTGGCGCGCAATTGACGCTTTGGAGAGTCCA 114
Db 16 AaPTpGluLyAspGluProGln-----CysCysLeuGluGlyPro 29
QY 115 AAGGTGAAGAAGCTTAAACCCGAAGAAATTCAGCATTCATGACCAAGATGCTG 174
Db 30 LySVaLlyAsnLeuAsnProLySlySpheSerLleHisAspGlnAspHislySVaLleu 49
QY 175 GTCTCGAGCTCTGGGAATTCATAGCAGTTCCAGATTAATAACTACATACGCCAGATC 234
Db 50 ValLeuAspSerGlyAsnLeuLeaValProAspLyAsnTyrlleArgProGluIle 69
QY 235 TTTCTTGCAATGACCTTCATCCTTGAGCTCAGCCTCGCGAAGAAAGAAAGTTC 294
Db 70 PhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGluLySglYserProIleLeu 89
QY 295 CTGGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGCAAGTCA 354
Db 90 LeuGlyValSerlySglYgluPheCysLeuTyrcyAspLyAspLySglYgluInserrHis 109
QY 355 CCATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTGGCTGCCAAAAGAAATCAGA 414
Db 110 ProSerLeuGlnLeuLySglYgluPheCysLeuTyrcyAspLyAspLySglYgluInserrHis 129
QY 415 CGCGGCGCTTCATCTTTTATAGGGCTCAGGTGGGCTCTCTGAAACATGCTGAGTGGGG 474
Db 130 ArgArgProPheLlePheTyArgAlaGlnValGlySerTyrPasmheCysLeuGlnSerAla 149
QY 475 GCTCAACCCGAGATGTTCACTGACCTCTGCAATTGATGAGCTGTGGGGTGA 534
Db 150 AlaHisProGlyTyrPheLleCysThrSerCysAsnCyAsnGlnProValGlyValThr 169
QY 535 GATTAATTTGAGAACAGAAACACATGATTTTCAACCAAGTTCGAAAGCTGAA 594
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Db 170 AsplvBphgEglnuBnrglyshisllEglnuPheSerPheglnuProValCyslyBAlaGlu 189
Qy 595 ATGAGCCCCAGTGAAGTCCAGCAT 618
Db 190 MetSerProSerGlnuValSerasp 197
RESULT 11
US-10-888-931-9
; Sequence 9, Application US/10888931
; Publication No. US20050013798A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECD DNAs AND POLYPEPT
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888, 931
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876, 790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-888-931-9

Alignment Scores:
Pred. No.: 7.04e-91 Length: 197
Score: 902.00 Matches: 172
Percent Similarity: 93.62% Conservative: 4
Best Local Similarity: 91.49% Mismatches: 6
Query Match: 79.54% Indels: 6
DB: 17 Gaps: 1

US-09-869-566-4 (1-650) x US-10-888-931-9 (1-197)

Qy 55 GACTAAGAGAGATGACCAAGCTTGGCGCCGCAATTGACCTCTTGCAGAGTCCA 114
Db 16 AsptTglnuLyasPgluProGln-----CyBcylEuglnuGlyPro 29
Qy 115 AAGTGAAGAACTTAACCGAAGAAATTGACATTCATGACAGGATCAAGAAAGTACTG 174
Db 30 LyBvalLyAsnLeuasnProlysluBpSerIlleHlaSpGlnuBphlslyBvalLeu 49
Qy 175 GTCTGAGACTCTGGGATCTCATGACAGTTCAGATTAATACTACATAGCCCAAGATC 234
Db 50 ValLeuAspSerGlyAsnLeuIlleAlaValProAspLyAsnTyrIlleArgProGluIle 69
Qy 235 TTCTTTGCAATTAGCCCTCATCTTGAAGCTCAGCTCTGCGGAGAAAGAGTCCGATTC 294
Db 70 PhePheAlaLeuAlaSerIleuSerIleuSerAlaSerAlaGlnuBgluysrProIleu 89
Qy 295 CTGGGGGTCTTAAGAGGAGTTTGTCTTACTGTGACAAGATTAAGAGCAAAATCAT 354
Db 90 LeuGlyValSerlyBgluBphecylBleuTyrCyAspLyAsnBpserlyBgluInsrHls 109
Qy 355 CCATCCCTTCACTGAAGAGAGAAAGTGAAGCTGCTGCGCCCAAAAGATCAGA 414
Db 110 ProSerLeuGlnuLeuylsBgluBphecylBleuTyrCyAspLyAsnBpserlyBgluInsrHls 129
Qy 415 CGCGGCGCTTCACTTTTATAGGCTCAGGTGGGCTCTGGAACATGCTGAGAGTGGCG 474
Db 130 ArgArgProPheIllePheTyrArgAlaGlnuValGlySerTyrAsnMetLeuGlnuSerAla 149
Qy 475 GCTCAACCCCGATGTTCATCTGACCTCTGCAATTGTATGAGCTGTGGGGTGAGA 534

Db 150 AlaHlsProGlyTyrPheIlleCysThrSerCyAsnCyAsnIluProValGlyValThr 169
Qy 535 GATTAATTTGAGAACGAGAAACATTTTTCATTTCAACAGTGGCAAGCTGAA 594
Db 170 AsplvBphgEglnuBnrglyshisllEglnuPheSerPheglnuProValCyslyBAlaGlu 189
Qy 595 ATGAGCCCCAGTGAAGTCCAGCAT 618
Db 190 MetSerProSerGlnuValSerasp 197

RESULT 12
US-09-788-963-6
; Sequence 6, Application US/09788963
; Patent No. US20020052473A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MCDONNELL, PETER C.
; APPLICANT: KUMAR, SANJAY
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
; FILE REFERENCE: GP-70607-1C1
; CURRENT APPLICATION NUMBER: US/09/788, 963
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/293,625
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/452,140
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 198
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-788-963-6

Alignment Scores:
Pred. No.: 4.22e-90 Length: 198
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: 9 Gaps: 0

US-09-869-566-4 (1-650) x US-09-788-963-6 (1-198)

Qy 112 CCAAGGTGAAGAACTTAACCGAAGAAATTGACATTCATGACAGGATCAAGAA 171
Db 30 ProLyBvalLyAsnLeuasnProlysluBpSerIlleHlaSpGlnuBphlslyBval 49
Qy 172 CTGCTCTGAGACTCTGGGATTCATGACAGTTCAGATTAATACTACATAGCCCAAG 231
Db 50 LeuValLeuAspSerGlyAsnLeuIlleAlaValProAspLyAsnTyrIlleArgProGlu 69
Qy 232 ATCTTCTTGAATTAGCCCTCATCTTGAAGCTCAGCTCTGCGGAGAAAGAGTCCGAT 291
Db 70 IlePhePheAlaLeuAlaSerIleuSerIleuSerAlaSerAlaGlnuBgluysrProIle 89
Qy 292 CTCTGGGGGTCTTAAGAGGAGTTTGTCTTACTGTGACAAGATTAAGAGCAAA 351
Db 90 LeuLeuGlyValSerlyBgluBphecylBleuTyrCyAspLyAsnBpserlyBgluInsr 109
Qy 352 CATTCATCCCTTCACTGAAGAGAGAAAGTGAAGCTGCTGCGCCCAAAAGATCA 411
Db 110 HlsProSerLeuGlnuLeuylsBgluBphecylBleuTyrCyAspLyAsnBpserlyBgluInsr 129
Qy 412 GCAGCCGCGCTTCACTTTTATAGGCTCAGGTGGGCTCTGGAACATGCTGAGAGTGC 471
Db 130 AlaArgArgProPheIllePheTyrArgAlaGlnuValGlySerTyrAsnMetLeuGlnuSer 149
Qy 472 GCGGCTCAACCCCGATGTTCATCTGACCTCTGCAATTGTATGAGCTGTGGGGTG 531
Db 150 AlaAlaHlsProGlyTyrPheIlleCysThrSerCyAsnCyAsnGlnuProValGlyVal 169

QY 532 ACAGATAATTGAGACGAGAAACATTTGATTTTCACACGATTCGAAAGCT 591
DB 170 TTTAspLysPheGluAsnArgLysHisIleGluPheSerPheGlnProValCysIlySala 189
QY 592 GAAATGAGCCCGAGTGGATCGCGAT 618
DB 190 GluMetSerProSerGluValSerAsp 198

RESULT 13
US-09-788-963-2
; Sequence 2, Application US/09788963
; Patent No. US20020052473A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MCDONNELL, PETER C.
; APPLICANT: KUMAR, SANJAY
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
; FILE REFERENCE: GP-70507-1C1
; CURRENT APPLICATION NUMBER: US/09/788,963
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/293,625
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/452,140
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-788-963-2

Alignment Scores:
Pred. No.: 4,35e-90 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: Gaps: 0

US-09-869-566-4 (1-650) x US-09-788-963-2 (1-218)

QY 112 CCAAGGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACGATCACAAGTA 171
DB 50 ProlYsValLysAsnLeuAsnProLysPheSerIleHisAspGlnAspHisVal 69
QY 172 CTGGTCTCGAAGCTCGGAATCTCATAGCACTCCGATTAACATCACTAGCCCGAG 231
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89
QY 232 ATCTTCTTTGCAATTAGCTCATCTGATCTGAGCTGCGGAGAAAGAAATCGATT 291
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnLysGlySerProIle 109
QY 292 CTCTCGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGATAAGCAAGT 351
DB 110 LeuLeuGlyValSerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129
QY 352 CATCCATCCCTTCAGCTGAAGAAAGAAAGAACTGATGAGCTGCGCAAAAGAAATCA 411
DB 130 HisProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaIleGlnLysGlnSer 149
QY 412 GCAGCGCGGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGCAACATGCTGAGTGC 471
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrAsnMetLeuGlnSer 169
QY 472 GCGGCTCACCCCGAGATGTTTCATCTGACCTCTCGCAATTGATGAGCTGTGGGGTG 531
DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnSerProValGlyVal 189
QY 532 ACAGATAATTGAGACGAGAAACATTTGATTTTCACACGATTCGAAAGCT 591
DB 190 TTTAspLysPheGluAsnArgLysHisIleGluPheSerPheGlnProValCysIlySala 209

QY 592 GAAATGAGCCCGAGTGGATCGCGAT 618
DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 14
US-09-876-790-8
; Sequence 8, Application US/09876790
; Publication No. US20030091532A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John B.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa U.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTID
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-790-8

Alignment Scores:
Pred. No.: 4,35e-90 Length: 218
Score: 895.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.92% Indels: 0
DB: Gaps: 0

US-09-869-566-4 (1-650) x US-09-876-790-8 (1-218)

QY 112 CCAAGGTGAAGAACTTAAACCCGAAAGAAATTGACATTCATGACGATCACAAGTA 171
DB 50 ProlYsValLysAsnLeuAsnProLysPheSerIleHisAspGlnAspHisVal 69
QY 172 CTGGTCTCGAAGCTCGGAATCTCATAGCACTCCGATTAACATCACTAGCCCGAG 231
DB 70 LeuValLeuAspSerGlyAsnLeuIleAlaValProAspLysAsnTyrIleArgProGlu 89
QY 232 ATCTTCTTTGCAATTAGCTCATCTGATCTGAGCTGCGGAGAAAGAAATCGATT 291
DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlnLysGlySerProIle 109
QY 292 CTCTCGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAAAGATAAGCAAGT 351
DB 110 LeuLeuGlyValSerLysGlyGluPheCysLeuTyrCysAspLysAspLysGlyGlnSer 129
QY 352 CATCCATCCCTTCAGCTGAAGAAAGAAAGAACTGATGAGCTGCGCAAAAGAAATCA 411
DB 130 HisProSerLeuGlnLeuLysLysGlyLysLeuMetLysLeuAlaIleGlnLysGlnSer 149
QY 412 GCAGCGCGGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGCAACATGCTGAGTGC 471
DB 150 AlaArgArgProPheIlePheTyrArgAlaGlnValGlySerTyrAsnMetLeuGlnSer 169
QY 472 GCGGCTCACCCCGAGATGTTTCATCTGACCTCTCGCAATTGATGAGCTGTGGGGTG 531
DB 170 AlaAlaHisProGlyTyrPheIleCysThrSerCysAsnGlnSerProValGlyVal 189
QY 532 ACAGATAATTGAGACGAGAAACATTTGATTTTCACACGATTCGAAAGCT 591
DB 190 TTTAspLysPheGluAsnArgLysHisIleGluPheSerPheGlnProValCysIlySala 209

QY 592 GAAATGAGCCCGAGTGAGTCAGCGAT 618
 DB 210 GluMetSerProSerGluValSerAsp 218

RESULT 15

US-10-139-833-12
 ; Sequence 12, Application US/10139833
 ; Publication No. US20030004106A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saria, Christiaan M.
 ; APPLICANT: Giles, Jennifer
 ; APPLICANT: Mu, Sharon X.
 ; APPLICANT: Xia, Min
 ; APPLICANT: Bass, Michael B.
 ; APPLICANT: Cravetto, Roger
 ; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist-Related Molecules and
 ; TITLE OF INVENTION: Uses Thereof
 ; FILE REFERENCE: 00-1213-E
 ; CURRENT APPLICATION NUMBER: US/10/139,833
 ; CURRENT FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: 60/170,191
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: 60/188,053
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: 60/194,521
 ; PRIOR FILING DATE: 2000-04-04
 ; PRIOR APPLICATION NUMBER: 60/195,910
 ; PRIOR FILING DATE: 2000-04-10
 ; PRIOR APPLICATION NUMBER: 09/724,583
 ; PRIOR FILING DATE: 2000-11-28
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: Patencin Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 218
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-139-833-12

Alignment Scores:
 Pred. No.: 4.35e-90 Length: 218
 Score: 895.00 Matches: 169
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.92% Indels: 0
 DB: 14 Gaps: 0

US-09-869-566-4 (1-650) x US-10-139-833-12 (1-218)

QY 112 CCAAGGTGAGAACTTAACCGAAGAAATTCAGCATTCATGACCGAGATCAAAAGTA 171
 DB 50 ProlySvalIyAbnLeuabnProlySlySpheSerIleHisapGlnaspHislyVal 69
 QY 172 CTGGTCTTGAGACTCTGGGAATCTCATAGCAGTTCAGATMAAACTACATACGCCAGAG 231
 DB 70 LeuValIleuaspSerGlyabnLeuIleValProaspIyAsnTyrlIearProGln 89
 QY 232 ATCTTCTTTGATTAAGCCTCATCTTGAGCTCAGCCTCTGCCGAGAAAGAAATCCGATT 291
 DB 90 IlePhePheAlaLeuAlaSerSerLeuSerSerAlaSerAlaGlySerProIle 109
 QY 292 CTCTGAGGGGCTCTTAAGAGGAGTTTGTCTCTACTGACCAAGGATTAAGACAAAGT 351
 DB 110 LeuLeuGlyValSerIyabGlyIubheCybLeuTyrcyAspIyabpIyabGlyIubSer 129
 QY 352 CATCCATCCCTTCAGCTGAGAGAGAGAAAGAACTGATGAAGCTGCTGCCAAAAGGAATCA 411
 DB 130 HisProSerLeuGlnLeuIyabGlyIubIyabLeuAlaIleGlnIyabGlnSer 149
 QY 412 GACAGCCCGGCTCTTATAGGGCTCAGGTGGGCTCTTGGAACATGCTGGAGTGG 471
 DB 150 AlaArgArgProPheIlePheTyArgAlaGlnValGlySerTrpAsnMetLeuGlnSer 169
 QY 472 GCGGCTACCCCGAGATGGTTCATCTGACCTCTCGCAATGTAAATGAGCGCTTGGGGTG 531

DB 170 AlaAlaHisProGlyTrpPheIleCystrSerCyAsnCyAsnGlnProValGlyVal 189
 QY 532 ACAGATTAATTTGAGAACCGAAGCACTTGAATTTTCATTCAACCGATTGGCAAGCT 591
 DB 190 ThrAspIyabPheGlnabnArgIyabHisIleGlnIubheSerPheGlnProValCysIySAla 209
 QY 592 GAAATGAGCCCGAGTGAGTCAGCGAT 618
 DB 210 GluMetSerProSerGluValSerAsp 218

Search completed: May 28, 2005, 17:43:59
 Job time : 76 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus.rnp model

Run on: May 28, 2005, 16:28:55 ; Search time 95.5 Seconds
(without alignments)
6970.711 Million cell updates/sec

Title: US-09-869-566-4
Perfect score: 1134
Sequence: 1 taaatcaccatgctgcact.....cgactctagagatcccg99 650

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 segs, 512079187 residues
Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2.1/USPTO.epool_p/US09869566/runat_27052005_163130_19910/app_query.faeta_1.839
-DB=UniProtc_03 -QFMT=Isaetan -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=human40.cdi -LIST=45
-OCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09869566 @CNCN_1_1_152 @runat_27052005_163130_19910 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEBUFFER -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONELOG
-BEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	895	78.9	218	1	IIF7_HUMAN	Q9N2H6 homo sapien
2	848	74.8	219	2	Q7RU00	Q7RU00 homo sapien
3	229.5	20.2	169	1	IIF9_HUMAN	Q9N2H8 homo sapien
4	229.5	20.2	169	2	Q7RTZ9	Q7RTZ9 homo sapien
5	229	20.2	157	2	Q7RTZ7	Q7RTZ7 homo sapien
6	212	18.7	158	1	IIF6_HUMAN	Q9N2H7 homo sapien
7	212	18.7	158	2	Q7RTZ8	Q7RTZ8 homo sapien
8	199	17.5	183	1	IIF8_MOUSE	Q9N2H6 mus musculi
9	191.5	16.9	156	1	IIF5_MOUSE	Q9N2H7 mus musculi
10	190	16.8	134	2	Q6UVX7	Q6UVX7 mus musculi
11	174.5	15.4	155	1	IIF5_HUMAN	Q9N2H8 homo sapien
12	174.5	15.4	155	2	Q7RTZ6	Q7RTZ6 mus musculi
13	174.5	15.4	164	1	IIF9_MOUSE	Q9N2H7 mus musculi
14	173	15.3	159	2	Q8CGA1	Q8CGA1 mus musculi
15	171	15.1	160	1	IIF6_MOUSE	Q9N2H8 mus musculi
16	167	14.7	178	1	IIIX_MOUSE	P25085 mus musculi

17	165.5	14.6	152	1	IIFA_MOUSE	Q8R459 mus musculi
18	158.5	14.0	159	2	Q7RTZ4	Q7RTZ4 homo sapien
19	158.5	14.0	177	1	IIIX_HUMAN	P18510 homo sapien
20	156.5	13.8	152	1	IIFA_HUMAN	Q8W21 h interieuk
21	156.5	13.8	152	2	Q7RTZ5	Q7RTZ5 homo sapien
22	156.5	13.8	267	2	Q73909	Q73909 gallus galli
23	154.5	13.6	177	1	IIIX_RABIT	P26890 oryctolagus
24	152	13.4	174	1	IIIX_BOVIN	P27482 bos taurus
25	151	13.3	176	1	IIIX_CANFA	Q9B6D0 canis famli
26	150	13.2	177	1	IIIX_TURTR	Q9B6D4 turtrlops tr
27	149	13.1	272	2	Q9DDF2	Q9DDF2 cyprinus ca
28	148	12.9	177	2	Q866R8	Q866R8 macaca fasc
29	146.5	12.9	177	1	IIIX_PIG	Q29056 sus scrofa
30	146.5	12.8	178	1	IIIX_RAT	P25086 rattus norv
31	145.5	12.8	272	2	Q8AXV9	Q8AXV9 carassius a
32	139.5	12.3	272	2	Q712J8	Q712J8 carassius a
33	137.5	12.1	177	1	IIIX_HORSE	Q18999 equus cabal
34	137.5	12.1	272	2	Q9DDF3	Q9DDF3 cyprinus ca
35	136	12.0	273	2	Q7T056	Q7T056 brachydanio
36	135.5	11.9	267	2	Q29082	Q29082 sus scrofa
37	132.5	11.7	211	2	Q7YS41	Q7YS41 sus scrofa
38	131.5	11.6	266	1	IIIB_SHEEP	P21651 ovib aries
39	129.5	11.4	276	2	Q57398	Q57398 cyprinus ca
40	129.5	11.4	276	2	Q9PW18	Q9PW18 cyprinus ca
41	128.5	11.3	238	2	Q8AXV8	Q8AXV8 carassius a
42	127.5	11.2	82	2	Q6PUJ3	Q6PUJ3 sus scrofa
43	121.5	10.7	267	1	IIIB_PIG	P26889 sus scrofa
44	121	10.7	268	1	IIIB_RAT	Q63284 rattus norv
45	120.5	10.6	269	1	IIIB_MOUSE	P10749 mus musculi

ALIGNMENTS

RESULT 1
IIF7_HUMAN
ID IIIF7_HUMAN STANDARD; PRT; 218 AA.
AC Q9N2H6; Q8TFD04; Q8TD05; Q9HBF2; Q9HBF3; Q9UHA6;
AD 28-FEB-2003 (Rel. 41) Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin 1 family member 7 precursor (II-1F7) (interleukin-1 zeta)
DE (II-1 zeta) (Fili zeta) (interleukin-1 homolog 4) (II-1H4)
DE (interleukin-1-related protein) (II-1RP1) (II-1X protein).
GN Name=IIIF7; Synonyms=FIILZ, IL1H4, IL1RP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Fetal B-cell, Fetal colon, Fetal lung, and Fetal testis;
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griewold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RT J. Biol. Chem. 275:10308-10314(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Colon carcinoma;
RA Manoj P.P., Mantovani A., Muzio M.;
RA Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS B AND C), SEQUENCE OF 46-54, AND VARIANTS
RP VAL-31 AND ALA-42.
RX MEDLINE=21066552; PubMed=1145836; DOI=10.1006/cyto.2000.0799;
RA Pan G., Riser P., Mo W., Baldwin D.T., Zhong A.W., Pilveroff E.,
RA Yaneura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandien R.;
RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-
RT 1R.";
RN [4]
CYtokine 13:1-7(2001).

RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE:20092888; PubMed:10625660; DOI=10.1074/jbc.275.2.1169;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Rubin M., Garika K.E.,
 RA Sims J.E.;
 RT "Four new members expand the IL-1 superfamily.";
 RL J. Biol. Chem. 275:1169-1173(2000).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS D AND E).
 RX MEDLINE:2198051; PubMed:1191773; DOI=10.1006/geno.2002.6752;
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
 RT "Genomic organization of the interleukin-1 locus.";
 RL Genomics 79:726-733(2002).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM B), AND VARIANTS VAL-31 AND ALA-42.
 RX TISSUE=Placenta;
 MEDLINE:23288257; PubMed:12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan D.C., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez Y., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Bottrighe A.Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Binds to Interleukin-18 receptor (IL-18R) receptor but
 not to IL-1 receptor. Could be a new player in the inflammatory
 and immune responses mediated by the IL-18/IL-18R axis.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=B;
 CC IsoId=Q9NZH6-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=Q9NZH6-2; Sequence=VSP_002653;
 CC Name=C;
 CC IsoId=Q9NZH6-3; Sequence=VSP_002656;
 CC Name=D;
 CC IsoId=Q9NZH6-4; Sequence=VSP_002654;
 CC Name=E;
 CC IsoId=Q9NZH6-5; Sequence=VSP_002655;
 CC -1- TISSUE SPECIFICITY: Isoforms A, B and C are expressed in testis,
 colon, placenta, lung and lymph node. Isoforms D and E were found
 only in testis and bone marrow. Whereas only isoform A is found in
 brain, only isoform B in kidney and only isoform C in heart.
 CC -1- INDUCTION: By phorbol ester (PMA) in different cell lines.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF200496; AAF69352.1; -;
 DR EMBL; AF167368; AAG29344.1; -;
 DR EMBL; AF251118; AAG14420.1; -;
 DR EMBL; AF251120; AAG14422.1; -;
 DR EMBL; AF251119; AAG14421.1; -;
 DR EMBL; AF201832; AAF25212.1; -;

DR EMBL; AY071840; AAL67151.1; -;
 DR EMBL; AY071841; AAL67154.1; -;
 DR EMBL; BC020637; AAH20637.1; -;
 DR HSSP; P18510; IL1R.
 DR Genew; HGNC:15563; IL1F7.
 DR H-InvDB; HIX0002387; -;
 DR MIM; 605510; -;
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005149; F:interleukin-1 receptor binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR008996; CytoK IL1 like.
 DR InterPro; IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR PRINTS; PR00264; INTERLEUKIN1.
 DR ProDom; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR SMART; PS00253; INTERLEUKIN_1; FALSE_NEG.
 DR Alternative splicing; Cytokine; direct protein sequencing;
 KW Multigene family; Polymorphism.
 FT PROPEP 1 45
 FT CHAIN 46 218
 FT VARSPPLIC 1 49
 FT VARSPPLIC 28 49
 FT VARSPPLIC 28 49
 FT VARSPPLIC 28 88
 FT VARSPPLIC 49 89
 FT VARSPPLIC 31 31
 FT VARIANT 42 42
 FT SEQUENCE 218 AA; 24126 MW; 96B089310D2CBA68 CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 3 01e-81 Length: 218
 Score: 895.00 Matches: 169
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.92% Indels: 0
 DB: 1 Gaps: 0
 US-09-869-566-4 (1-650) x 11F7_HUMAN (1-218)
 QY 112 CCAAGGTGAGAACTTAAACCGAAGAAATTCAGCATTCATGACGAGATCAAGTA 171
 DB 50 ProlysVallylAsnleuasnProlyslsPheserlleHisAspGlnasphlslyVal 69
 QY 172 CTGGTCTGAGCTCTGGGGAATCTCATAGAGATTCAGATTAATAACTACATAGCCCAAG 231
 DB 70 LeuValleuAspSerGlyAsnleuIleAlaValProAspLyAsnIlyrilleArgProGlu 89
 QY 232 ATCTTCTTGATTTAGCCCTCATCTTCTGAGCTCAGCTCGCGAAGAAAGATTCGATT 291
 DB 90 llePhePheAlaLeuAlaSerSerleuSerAlaSerAlaGlnylserProIle 109
 QY 292 CTCCTGGGGGTCTTAAAGGAGATTTGTCTCTACTGTGACAGATTAAGACAAAGT 351
 DB 110 LeuLeuGlyValSerIlyserIlyGlnPheCysleuIlyrCysAspLyAspIlyserGlnSer 129
 QY 352 CATTCATCCCTTCAGCTGAAGAGAACTGATGAGAGCTGGCTGCCCAAGAAATTA 411
 DB 130 HisProSerleuGlnleuIlyserGlyIlyleuMetIlyleuAlaGlnylserGlnSer 149
 QY 412 GCAAGCGGCGCTTCATCTTTATAGGGCTCAGGTGGCTCTCGAACAATGCTGAGAGTGG 471
 DB 150 AlaArgArgProPheIlePheIlyrArgAlaGlnValGlySerIlyrPasnMetleuGlnSer 169


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US-09-869-566-4 (1-650) x Q7RU00 (1-219)
QY 55 GACTACAAAGACATGACGCAAGCTTGG-----GCCGCGAATTCAAGCTTTGCG 105
Db 16 APTTPGILuysapoinProGInCysCysleuGluAspProkIaIySerProleuGlu 35
QY 106 AGAGGTCCA-----AAGGTGAAGACTTA 129
Db 36 ProGILyProSerleuProTherMetAenPheValIeThSerArgySVallySerleu 55
QY 130 AACCCGAAGAAATTCGATTCATGACCGAGATCAAGAAATCTGCTTCGACTTGGG 189
Db 56 AaNProluylapheSerIleHsaPGLInAsPheIlyValIeuValIeuAspSerGly 75
QY 190 AATCTCATGACGATTCAGATTAAGAACTACATACGCCGAGATCTCTTTGATTAAGC 249
Db 76 AaHueIleIaIaValIProAspIlySaenIlyIleArgProGILuIlePheheIaIeuaIa 95
QY 250 TCATCTTGAAGCTCAGCTCTCTCGGAGAAAGAAAGTCCGATTCCTCGGGGCTCTTAA 309
Db 96 SerSerleuSerSerIaSerIaIaGluIuylGlySerleuIleleuGluGlyValSerIys 115
QY 310 GGGGAGTTTGTCTTCTACTGTGACAAAGATTAAGCAAGATCATTCCTTCAGCTG 369
Db 116 GILyGluPheCysleuIyrcysAspIlySAspIlySgILyGlnSerIisProSerleuGlnIeu 135
QY 370 AAGAAGAGAAATCTGATGAAGCTGGCCCAAGAAAGATTCAGACGCCGCTTCATC 429
Db 136 IySILySgILySleuIySleuIaIaGILySgILySerIaIaArgIArgProPheIle 155
QY 430 TTTTATAGGCTCAGGTGGCTCTCGAAATGCTGAGTCCGCGGCTCACCCGGATG 489
Db 156 PheIyArgIaGILyIaGILyIaGILySerIaGAsnMetleuGILySerIaIaIaIisProGlyTTP 175
QY 490 TTCATTCGACCTCCCGCAATTTGATGAGCTGTGGGGTGACAGATTAATTTGGAGC 549
Db 176 PheIleCysIhSerCysAsnGILyProIaGILyValThraPlySProGILyuaIn 195
QY 550 AGAAACACATTAATTTTCATTCAACCA---GTTTGAAAGCTGAATGAGCCCACT 606
Db 196 ArgIyShIleIleGILySleuSerPheGILyProIaValCyluYalIaGILyMetSerProSer 215
QY 607 GAGGTCCAGCAT 618
Db 216 GILyValSerAsn 219

RESULT 3
ID 11F9_HUMAN STANDARD; PRT; 169 AA.
AC Q9NZH8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin 1 family member 9 (IL-1F9) (Interleukin-1 homolog 1) (IL-1H1) (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1 related protein 2) (IL-1RP2).
GN Name=IL1F9; Synonyms=IL1E, IL1H1, IL1RP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]

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RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Epithelium;
RX MEDLINE=21359532; PubMed=11466363;
RA Debats R., Timane J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kappa B activation through the
RT orphan IL-1 receptor-related protein 2.";
RL J. Immunol. 167:1440-1446(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
RA Bustfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2.";
RL Genomics 66:213-216(2000).
CC -I- FUNCTION: Function as an agonist of NF-kappa B activation through
CC the orphan IL-1-receptor-related protein 2. Could constitute part
CC of an independent signaling system analogous to interleukin-1
CC alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1
CC receptor type I (IL-1RI), that is present in epithelial barriers
CC and takes part in local inflammatory response.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Highly expressed in tissues containing
CC epithelial cells; skin, lung, stomach and esophagus. In skin is
CC expressed only in keratinocytes but not in fibroblasts,
CC endothelial cells or melanocytes. Up-regulated in lesional
CC psoriasis skin.
CC -I- INDUCTION: By TNF-alpha and by IFN-gamma in keratinocytes.
CC -I- SIMILARITY: Belongs to the IL-1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sb.ch/announce/
CC or send an email to license@isb-sb.ch).
DR EMBL: AF200492; AAF69248.1; -.
DR EMBL: AF206696; AAG35670.1; -.
DR HSSP: P18510; IL1F9.
DR Genew; HGNC:15741; IL1F9.
DR MIM: 605542; -.
DR GO: GO:0007267; P:cell-cell signaling; TAS.
DR CO: GO:0009613; P:response to pest/pathogen/parasite; TAS.
DR InterPro; IPR008996; CytoK_IL1_Like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR ProDom; PDD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; FALSE_NEG.
KW Cytokine; Multigene family.
SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Alignment Scores:
Pred. No.: 3,95e-14 Length: 169
Score: 229.50 Matches: 56
Percent Similarity: 53.12% Conservative: 29
Best Local Similarity: 35.00% Mismatches: 62
Query Match: 20.24% Indels: 13
DB: 1 Gaps: 5

US-09-869-566-4 (1-650) x 11F9_HUMAN (1-169)
QY 64 GACTACGACGCAAGCTTGGCGCGCAATTCAGCTCTTTGAGAGGTCCAAAGGTGAAG 123
Db 7 AaPalaabpGILyGILyArgIaIaValIyrcGlnSerMetCyluS- 21
QY 124 AACTTAACCCGAGAAATTCAGATTCATGACGAGATCAAGAAAGTACTGCTCGAC 183

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Db 22 -----ProIleThrglyThrIleAsnAspLeuAsnIleValTrpThrLeuGln 38
 QY 184 TCTGGGAATCTCTACAGTTCAGATTAATAAATACTACAGCCCAAGATCTTCTTGA 243
 Db 39 GlyAlaAsnLeuValAlaValProArgSerAspSerValThrProValAlaVal 58
 QY 244 TTAGCCTCATCCCTGAGCTCAGCTCGAGAG---AAAGAGAGTCCGATTCCTCGGG 300
 Db 59 IleThCyluSerThrProGluAlaLeuGlnGlnGlyArgGlyAspProIleThrLeuGly 78
 QY 301 GTCCTTAAAGGGAGTTTGTCTCTACTGACAGATTAAGACAAATCATCCATCC 360
 Db 79 IleGlnAsnProGluMetCysLeuThrCysGluIuValGlyGln-----ProThr 96
 QY 361 CTTTCAAGAGAGAGAGAACTGATGAAGCTGCGCCCAAGAAATCAGACCCGG 420
 Db 97 LeuGlnLeuLeuGlnIleuIuLysIleMetAspLeuThrGlyIuProGluProVal---Lys 115
 QY 421 CCTTCATCTTTATATAGGCTCAGTGGCTCTGGAACAATGCTGAGTGGCGCTCAC 480
 Db 116 ProPheLeuPheThrGlyArgAlaLysThrGlyArgThrSerThrLeuIuSerValAlaPhe 135
 QY 481 CCCGATGCTTCACTGACCTCTGCAATGTATAGAGCTTGTGGGTTGACAGATAA 540
 Db 136 ProArgThrPheIleLeuLeuSer---LysArgAspGlnProIleIleuThrSerGlu 154
 RESULT 4
 QRTZ9 PRELIMINARY; PRT; 169 AA.
 ID QRTZ9; 01-MAR-2004 (TREMBLrel. 26, Created)
 AC QRTZ9; 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE IL-1F9 (IL-1H1, IL-1RP2, IL-1-epsilon).
 GN Name=IL1F9;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20545212; PubMed=11093146;
 RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
 RA Barton J.L., Herbert R., Bosisio D., Higgins L., Nicklin M.J.;
 RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
 RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities";
 RL Eur. J. Immunol. 30:3299-3308(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
 RA Notwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
 RA Gierlich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,
 RA Hildebrandt F.;
 RT "Molecular cloning of the interleukin-1 gene cluster: construction of
 RT an integrated YAC/PAC contig and a partial transcriptional map in the
 RT region of chromosome 2q13";
 RL Genomics 41:370-378(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94425215; PubMed=8188271;
 RA Nicklin M.J.H., Weith A., Duff G.W.;
 RT "A physical map of the region encompassing the human interleukin-1
 RT alpha, interleukin-1-beta and interleukin-1 receptor genes";
 RL Genomics 19:382-384(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
 RA Korman K.;
 RT "A sequence-biased map of the nine genes of the human interleukin-1
 RT cluster";
 RL Genomics 79:718-725(2002).

RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/dbrc.1999.1440;
 RA Mulero J.J., Pace A.M., Nelson S.T., Loeb D.D., Correa T.R.,
 RA Dimaac R., Ford J.E.;
 RT "IL1HY1: A novel interleukin-1 receptor antagonist gene";
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Rubin M., Garza K.E.,
 RA Sims J.E.;
 RT "Four new members expand the interleukin-1 superfamily";
 RL J. Biol. Chem. 275:1169-1175(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
 RA Griewold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.;
 RT "Identification and initial characterization of four novel members of
 RT the interleukin-1 family";
 RL J. Biol. Chem. 275:10308-10314(2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2";
 RL Genomics 66:213-216(2000).
 RN [9]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2106552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
 RA Pan G., Rieber P., Mao W., Baldwin D.T., Zhong A.W., Flivartoff B.,
 RA Yaneura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.;
 RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
 RT 1Rp";
 RL Cytokine 13:1-7(2001).
 RN [10]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
 RA Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fusell J.,
 RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
 RT "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
 RT member";
 RL J. Biol. Chem. 276:20597-20602(2001).
 RN [11]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21359532; PubMed=11466363;
 RA Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
 RA Kastelein R.A.;
 RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kB activation through the orphan
 RT IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446";
 RL J. Immunol. 167:1440-1446(2001).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;
 RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,
 RA Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G.,
 RA Pan Y., Smith D.E., Young P.R.;
 RT "A new nomenclature for the IL-1-family genes";
 RL Trends Immunol. 22:536-537(2001).
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an
 CC EMBL/GenBank/DDJ third party annotation (TPA) entry.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 DR EMBL; BN000002; CAD2874.1; -.
 DR HSP; P18510; I1IR.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005152; P:interleukin-1 receptor antagonist activity; IEA.
 DR GO; GO:0006955; P:immune response; IEA.

DR	InterPro; IPR008996; Cytok IL1 like.
DR	InterPro; IPR003297; InterleukinIL1A.
DR	InterPro; IPR000975; Interleukin_1.
DR	Pfam; PF00340; IL1; 1.
DR	PRINTS; PR00264; INTERLEUKIN1.
DR	PRINTS; PR01360; INTERLEUKINIX.
DR	Prodrom; PD002536; Interleukin_1; 1.
SQ	SEQUENCE 169 AA; 18721 MW; _F0DA9243706FA154 CRC64;

Alignment Scores:		3,95e-14	Length: 169
Score:	229.50	Matches: 56	
Percent Similarity:	53.12%	Conservative: 29	
Best Local Similarity:	35.00%	Mismatches: 62	
Query Match:	20.24%	Indels: 13	
DB:	2	Gaps: 5	

US-09-869-566-4 (1-650) x Q7RTZ9 (1-169)	
Qy	64 GACGATAGCAGCAAGCTTGGCGCCGCAGATTCACTCTTTGACAAAGTCGAAG 123
Dd	7 AspaIaaSpqIgiYgiYArGaLaValaTyriGInsermetCysLys----- 21
Qy	124 AACTTAACCAGGAAMAATTGAGCATTCAGCACAGGATCAACAAGTACTGTCTTGAC 183
Dd	22 -----ProIethrGlyThrlEshnAspLeuSnngInGlnValTTrPThrLeugIn 38
Qy	184 TCTGGGATCTCATGACGAGTTCCAGATAAAAATCAATACGCCAGAGATCTTTGCA 243
Dd	39 GlyInsnLeuValAlaIvalProrXSerAspSerValThrProValThrAlaIal 58
Qy	244 TTAGCTTCATCTTGAGCTACGCTCTGGCGAG--AAAGAAGTCGATTTCTTGGG 300
Dd	59 IleHrcCysLysTYrProGlualLeuGlnIdmlYarGglYaSPProIIeryrLeugLy 78
Qy	301 GTCTCTAAAGGGAGTTTGTCTACTCTGTGACAAAGATVAAAGAACAAAGTCATCC 360
Dd	79 IlEgLnAsnpProGIumetCysLeuTYrCYSeLUySVaIGlYgIn----Prothr 96
Qy	361 CTTCAGCTGAAGAGAGAGAAATCATGAAAGCTGGCTGCCCAAAGATCAGACGCCG 420
Dd	97 LeuGInleuYsgUgnInLYslIleMeCaSpLeuTYrGLYgInProGluProVal--Lys 115
Qy	421 CCTTCATCTTTTAAATAGGCGCTCAGAGTGCGCTCTTGAAACATGCTGAGTGGCGGCTCAC 480
Dd	116 ProheLuEnPhetyrArgGalalyThrdLYrGrhSerThrLeuGInSerValAlaIaphe 139
Qy	481 CCCGAGATGTTCACTGACACCTCTCGCAATTGTATAGCCTGTGTGGGGTGACGATAAA 540
Dd	136 ProbaspTrppheilelaIaSerSer--LysArgAspGlnProIIerleLeuthrSerGlu 154

RESULT 5	
Q7RTZ7	PRELIMINARY; PRT; 157 AA.
ID	Q7RTZ7
AC	Q7RTZ7;
DT	01-MAR-2004 (TREMBLrel. 26, Created)
DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	IL-1f8 (FILI-Heta).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX	NCBI_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RK	MEDLINE=20545212; PubMed=11093146;
RA	DOI=10.1002/1521-4141(200011)30:11<3299::AID-LMMJ3299>3.0.CO;2-S;
RA	Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.D.;
RT	"A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT	cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."
RL	Ext. J. Immunol. 30:3299-3308(2000).
RN	[2]
RP	SEQUENCE FROM N.A.

RX MEDLINE=77312633; PubMed=9169134; DOI=10.1006/geno.1997.4654;
 RA Nwachang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
 RA Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurrit D.M.,
 RA Hildebrandt F.,
 RT "Molecular cloning of the interleukin-1 gene cluster: construction of
 RT an integrated YAC/PAC contig and a partial transcriptional map in the
 RT region of chromosome 2q33."
 RL Genomics 41:370-378(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94245215; PubMed=8188271;
 RX MEDLINE=94245215; PubMed=8188271;
 RA Nicklin M.J.H., Weith A., Duff G.W.,
 RA Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G.,
 RA Korman K.,
 RT "A sequence-based map of the nine genes of the human interleukin-1
 RT cluster."
 RL Genomics 79:718-725(2002).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99433727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
 RX MEDLINE=99433727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
 RA Mulero J.J., Pace A.M., Nelson S.T., Loeb D.D., Correa T.R.,
 RA Dmanan R., Ford J.E.,
 RA "IL1H1: A novel interleukin-1 receptor antagonist gene";
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
 RN [6]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
 RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
 RA Sims J.E.,
 RT "Four new members expand the interleukin-1 superfamily."
 RL J. Biol. Chem. 275:1169-1175(2000).
 RN [7]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
 RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
 RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
 RA Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L.,
 RA Young P.R.,
 RT "Identification and initial characterization of four novel members of
 RT the interleukin-1 family."
 RL J. Biol. Chem. 275:10308-10314(2000).
 RN [8]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20318633; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RX MEDLINE=20318633; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.,
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2."
 RL Genomics 66:213-216(2000).
 RN [9]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21066552; PubMed=1145836; DOI=10.1006/cyto.2000.0799;
 RX MEDLINE=21066552; PubMed=1145836; DOI=10.1006/cyto.2000.0799;
 RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
 RA Yansura D., Lewis L., Eigenbrodt C., Henzel W.J., Vanden R.,
 RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
 RT 1RP."
 RL Cytokine 13:1-7(2001).
 RN [10]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21822953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
 RX MEDLINE=21822953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
 RA Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
 RA Pace A.W., Hansen D., Schweighofer K., Wize N.K., Ford J.E.,
 RT "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
 RT member."
 RL J. Biol. Chem. 276:20597-20602(2001).
 RN [11]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=21359532; PubMed=11466363;

QY 253 -----TCCGTGAGCTCAGCCCTCTGCGAGAAAGAAAGTCCGATTCCTGCGGGCTCTCT 306
DB 49 CysArgHisValIgluThrleugluysAspArgGlyAsnProIleTyrleuLeuAsn 68
QY 307 AAAGGGGACCTTTGCTGCTACGTGTCAGCAAGGATTAAGGCAAGATCATCCCTTCAG 366
DB 69 GlyLeuAsnLeucysLeuMetCysAlaIysValGlyAspGln-----ProThrleuGln 86
QY 367 CTGAAGAGAGAGAAATCAGTGAAGCTGGCTGCCCAAGAAAGAAATCAGCAGCGCGCCCTTC 426
DB 87 LeuIysGluIysAspIleMetAspLeuIyryaEngInProGluProVal---LysSerPhe 105
QY 427 ATCTTTTAAAGGCTCAGCTGGCTCTCTGGAACATCTGAGTGGCGGCTCAACCCGGA 486
DB 106 LeuPheTyrHisSerGlnSerGlyArgAsnSerThrPheGluSerValAlaPheProGly 125
QY 487 TGGTTCATCTGCAACCTCTGCAATTTGATAGCGCTGTGGGGTGACATTAATTTGAG 546
DB 126 TrpPheIleAlaValSerSerGluGlyGlyCysProLeuIleuThrGlnGlu-LeuG1 145
QY 547 AACAGGAAACACATTTGATTTT 568
DB 145 yIysAlaAenThrThraSphe 152
RESULT 7
QYRTZ8 PRELIMINARY; PRT; 158 AA.
AC QYRTZ8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IL-1P6 (PIL-1-eps11on).
GN Name=IL1P6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545212; PubMed=11093146;
DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RA Barton J.L., Herbert R., Bosisio D., Higgins L., Nicklin M.J.,
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
RA Notthang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
RA Gierlich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,
RA Hildebrandt F.;
RT "Molecular cloning of the interleukin-1 gene cluster: construction of
RT an integrated YAC/PAC contig and a partial transcriptional map in the
RT region of chromosome 2q13";
RL Genomics 41:370-378(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245215; PubMed=8188271;
RA Nicklin M.J.H., Weith A., Duff G.W.;
RT "A Physical map of the region encompassing the human interleukin-1-
RT alpha, interleukin-1-beta and interleukin-1 receptor genes";
RL Genomics 19:382-384(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
RA Nicklin M.J.H., Barton J.L., Nguyen W., Fitzgerald M.G., Duff W.G.,
RA Korman K.;
RT "A sequence-based map of the nine genes of the human interleukin-1
RT cluster";
RL Genomics 79:718-725(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
RA Mulero J.J., Pace A.M., Neiken S.T., Loeb D.D., Correa T.R.,
RA Drmanac R., Ford J.E.;
RT "IL1H1: A novel Interleukin-1 receptor antagonist gene";
RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four new members expand the interleukin-1 superfamily";
RL J. Biol. Chem. 275:1169-1175(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griewold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smucko J.S.,
RA Zhou H., Leiby K.R., Holmgren L.M., Geating D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the
RT IL-1 family on human chromosome 2";
RL Genomics 66:213-216(2000).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=2106552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
RA Pan G., Rasser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA Yanaura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.;
RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
RT 1R";
RL Cytokine 13:1-7(2001).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
RA Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J.,
RA Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT "Cloning and characterization of IL-1HY2, a novel interleukin-1 family
RT member";
RL J. Biol. Chem. 276:20597-20602(2001).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359532; PubMed=11466363;
RA Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
RA Wagner U., Edwards G., Clifford T., Menon S., Bazan J.F.,
RA Kastelein R.A.;
RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
RT as an antagonist and agonist of NF-kB activation through the orphan
RT IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.",
RL J. Immunol. 167:1440-1446(2001).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;
RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,
RA Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G.,
RA Pan Y., Smith D.E., Young P.R.;
RT "A new nomenclature for the IL-1-family genes";
RL Trends Immunol. 22:536-537(2001).
CC -1- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -1- SIMILARITY: Belongs to the IL-1 family.
DR EMBL; BR000002; CAD2875.1; -.
DR HSSP; O9QY1; 1MD6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR InterPro; IPR008996; CytoK_IL1-like.
DR InterPro; IPR003294; InterleukinIL1B.


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Db      5 SerGlyAlaLeuCyS-----PheArgMet 12
QY      151 CATGACCCAGATCACAAGATGCTGCTGSACTCGGAAATCTCATAGA-----GTT 204
Db      13 LysAspSerAlaLeuValLeuYrLeuH1AsnAsnGlnLeuValLeuGlyLeu 32
QY      205 CCAGATTAAGATACATACAGCCAGATCTTTGATAGGCTCATCTTGAAGCTCA 264
Db      33 H1sAlaGlnValLeuValLeuYrGlnGlnLeuValValProAsnArgAlaLeuAsp 52
QY      265 GCCTTCGCCGAGAAAGAAAGTCGATTCCTCGGGGCTCTTAAAGGGAATTTGCTTC 324
Db      53 AlaSerLeu-----SerProValIleLeuGlyValGlnGlyIleGlySerGlnCySLeu 69
QY      325 TACTGTGACAGAGTAAATGACAAAGTATCATCTCCCTTCACTGAAAGAAAGAACTG 384
Db      70 SerCyGlyThrGlnLeuYrGlnLeu-----ProIleLeuYrLeuGlnProValaenIle 86
QY      385 ATGAAGCTG---GCTGCCAAAGAAAGATGACGACGCGGCGCTTCATCTTTATAGGGCT 441
Db      87 MetGlnLeuYrLeuGlnGlyAlaYrGlnSer-----LysSerPheThrPheYrArgArg 104
QY      442 CAGGTGGGCTCCTGGAACATGCTGAGTGGCGGCTCACCCCGAGATGTTCACTGACCC 501
Db      105 AspMetGlyLeuThrSerSerPheGlnSerAlaAlaIleYrProGlyYrPheLeuCySThr 124
QY      502 TCCTGCATTTGATGACGCTGTGGGGTGACA 534
Db      125 SerProGlnAlaAspGlnProValArgLeuThr 135

RESULT 10
Q6UVX7 PRELIMINARY; PRT; 134 AA.
AC Q6UVX7;
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE IRA2.
DE ORFNames=UNQ2456;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
RA Seethagiri S., Simmons L., Singh J., Smith V., Stinson J., Vasta A.,
RA Vandlen R., Watanabe C., Weand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270(2003).
CC -1 SIMILARITY: Belongs to the IL-1 family.
EMBL: AY59111; AAC09469.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR003297; Interleukin1LRA.
DR InterPro: IPR000975; Interleukin_1.
DR PRINTS: PR00264; INTERLEUKIN1.
DR PRINTS: PR01360; INTERLEUKINX.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
SQ SEQUENCE 134 AA; 14928 MW; D5369C5AD44A9752 CRC64;

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Alignment Scores:
Pred. No.: 3,68e-10 Length: 134
Score: 190.00 Matches: 40
Percent Similarity: 64.778 Conservative: 17
Best Local Similarity: 45.458 Mismatches: 27
Query Match: 16.754 Indels: 4
DB: 2 Gaps: 3

US-09-869-566-4 (1-650) x Q6UVX7 (1-134)

QY      277 AAAGAAAGTCCGATTCCTCGGGGCTCTTAAAGGGAATTTGCTACTGTGCAAG 336
Db      36 ArgGlyAspProIleYrLeuGlnGlyIleGlnAsnProGlnMetCySLeuYrCySLeu 55
QY      337 GATTAAGACAAAGTATCATCTCCCTTCACTGAAAGAAAGAACTGATGAAGCTGCGT 396
Db      56 ValGlyGlnGln-----ProThrLeuGlnLeuYrGlnGlnYrIleMetAspLeuYr 73
QY      397 GCCAAAGAAAGATGACGACGCGGCGCTTCATCTTTATAGGGGCTCAGGTGGGCTCTCG 456
Db      74 GlyGlnProGlnProVal---LysProPheLeuPheYrArgAlaYrThrGlyArgThr 92
QY      457 AACATGCTGGAAGTCCGCGGCTCACCCCGAGATGTTCACTGACCTTCGCAATTGAA 516
Db      93 SerThrLeuGlnSerValAlaIlePheProAspTrpPheIleAlaSerSer---LysArgAsp 111
QY      517 GAGCCTGTTGGGGTGACAGATAA 540
Db      112 GlnProIleIleLeuThrSerGln 119

RESULT 11
I1F5 HUMAN
ID I1F5 HUMAN STANDARD; PRT; 155 AA.
AC Q9UEB0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE "Interleukin 1 family member 5 (IL-1F5) (interleukin-1 delta) (IL-1
DE delta) (Fli1 delta) (interleukin-1-like protein 1) (IL-1L1)
DE (interleukin-1 HX1) (IL-1HX1) (interleukin-1 receptor antagonist
DE homolog 1) (IL-1ra homolog 1) (IL-1 related protein 3) (IL-1RP3)
DE (UNQ1896/PRO4342).
GN Name=I1F5; Synonyms=FIL1D, IL1H1, IL1L1, IL1RP3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
RA Smith D.E., Ranshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RA Sims J.E.;
RT "Four new members expand the IL-1 superfamily.";
RT J. Biol. Chem. 275:1169-1175(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Petal skin;
RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA Dymnac R., Ford J.E.;
RT "IL1HY: a novel interleukin-1 receptor antagonist gene.";
RT Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20545212; PubMed=11093146;
RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J.H.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1
RT cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RT Eur. J. Immunol. 30:3299-3308(2000).

```

RN [4]
 RX SEQUENCE FROM N.A.
 RX MEDLINE=21359532; PubMed=11466363;
 RA Debers R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
 RA Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
 RA Kastelein R.A.;
 RA "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
 RT as an antagonist and agonist of NF-kappa B activation through the
 RT orphan IL-1 receptor-related protein 2.";
 RL J. Immunol. 167:1440-1446(2001).
 RN [5]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
 RA Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,
 RA Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
 RT "Identification and gene organization of three novel members of the
 RT IL-1 family on human chromosome 2.";
 RL Genomics 66:213-216(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [7]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshimiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Heltón E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grilmond J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalloe D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Is a highly and a specific antagonist of the IL-1
 CC receptor-related protein 2-mediated response to interleukin 1
 CC family member 9 (IL1F9). Could constitute part of an independent
 CC signaling system analogous to interleukin-1 alpha (IL-1A), beta
 CC (IL-1B) receptor agonist and interleukin-1 receptor type I (IL-
 CC 1R1), that is present in epithelial barriers and takes part in
 CC local inflammatory response.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in keratinocytes but
 CC also in fibroblasts, endothelial cells or melanocytes. Detected
 CC also in the spleen, brain leukocyte and macrophage cell types.
 CC Increased in lesional psoriasis skin.
 CC -1- INDUCTION: By phorbol ester (PMA) and Lypopolysaccharide (LPS)
 CC treatment in macrophage cell line.
 CC -1- SIMILARITY: Belongs to the IL-1 family.

```

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CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announcement/ib-sib.ch).
CC      or send an email to license@ib-sib.ch).
CC      -----
DR      EMBL; AF201830; AAF25210.1; -
DR      EMBL; AF186094; AAF02757.1; -
DR      EMBL; AJ242737; CAB59822.1; -
DR      EMBL; AJ242738; CAB59823.1; -
DR      EMBL; AJ271338; CAB67704.1; -
DR      EMBL; AF216693; AAF76981.1; -
DR      EMBL; AF230377; AAF91274.1; -
DR      EMBL; AY359117; AA089475.1; -
DR      EMBL; BC024747; AAH24747.1; -
DR      PIR; JC7104; JC7104.
DR      HSSP; P18510; 1ILR.
DR      Genew; HGNC:15561; IL1F5.
DR      MIM; 605507; -.
DR      GO; GO:0005155; F:interleukin-1 receptor antagonist activity; TAS.
DR      InterPro; IPR008996; CytoC IL1 like.
DR      InterPro; IPR009375; Interleukin_1.
DR      Pfam; PF00340; IL1; 1.
DR      PRINTS; PR00264; INTERLEUKIN1.
DR      ProDom; PD002536; Interleukin_1; 1.
DR      SMART; SM00125; IL1; 1.
DR      PROSITE; PS00253; INTERLEUKIN_1; 1.
KW      Cytokine; Multigene family.
SQ      SEQUENCE 155 AA; 16962 MW; B96DB5EPA2612E25 CRC64;
Alignment Scores:
Pred. No.: 1.38e-08 Length: 155
Score: 174.50 Matches: 54
Percent Similarity: 42.60% Conservative: 18
Best Local Similarity: 31.95% Mismatches: 48
Query Match: 15.39% Indels: 49
DB: 1 Gaps: 7
US-09-869-566-4 (1-650) x IL1F5_HUMAN (1-155)
QY      91 AATTGAGCTCTTTGGAGAGGTCCTCAAGGTGAAGAACTTAACCGAAGAAATTGACAGATT 150
DB      4 SerGlyAlaLeuCyS-----PheArgMet 11
QY      151 CATGACCAAGATCAACAAGTACTGCTGCTGACACTCTGGAAATCTCATAGCACTTCAGATT 210
DB      12 LysAspSerAlaLeuValLeuValLeuValLeuHisAsnAsnGlnLeu----- 26
QY      211 AAAAACTACATACGCCCGCAGAGATCTTTTGATTGATTGCTTACCTTCAGTCAAGCTCTT 270
DB      27 -----LeuAlaGlyLeuHisAlaGlyLys 35
QY      271 GCGGAGAAAGA-----AGT 285
DB      36 ValIleValGlyGlnGlnIleSerValValProAsnArgTyrLeuAspAlaSerLeuSer 55
QY      286 CGATTCCTCTGGGGGATCTCAAAAGGAGGAGTTTGCTCTACTGTCAGCAACAAGATAAAGA 345
DB      56 ProValIleLeuGlyValGlnGlnIleValSerGlnCybLeuSerCyS-----GlyValGly 73
QY      346 CAAGACTCATCCCTTCAGCTGAGTGAAGAGAAAGAAATGATGAAGCTG---GCTGCCCA 402
DB      74 Gln---GlnProThrLeuThrLeuGlnProValAsnIleMetGluLeuTyrLeuGlyAla 92
QY      403 AAGAATGACAGACGCCGCCCTTCATCTTTTATAGGCGCTCAAGTGGCGCTCTGGAACATG 462
DB      93 LysGlnSer-----LysSerPheThrPheTyrArgArgAspMetGlyLeuThrSer 110
QY      463 CTGAGAGTGGGGGGCTACCCCGGATGGTTCACTGCACTCTCGAAATTGTATAGAGCT 522

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DB 111 pHeGUseRvAlAlaTyRProGlyTRpHeLeuCyThrValProGluAlaSepInPro 130

QY 523 GTTGGGTCAGACATTAATTGGAGAC 549

DB 131 ValArgLeuThrGlnLeuProGluAen 139

RESULT 12

Q7RTZ6 PRELIMINARY; PRT; 155 AA.

AC 07RTZ6; 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE IL-1P5 (IL-1HY, FI1A-delta, IL-1RP3, IL-1L1, IL-1-delta).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxId=9606;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20545212; PubMed=11093146; DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMUJ3299>3.0.CO;2-S; Barton J.L., Herbst R., Bosisto D., Higgins L., Nicklin M.J., "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities."; Eur. J. Immunol. 30:3299-3308(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654; Notliwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J., Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M., Hildebrandt F.; "Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13."; Genomics 41:370-378(1997).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=94245215; PubMed=8188271; Nicklin M.J.H., Weich A., Duff G.W.; "A physical map of the region encompassing the human interleukin-1 alpha, interleukin-1-beta and interleukin-1 receptor genes."; Genomics 19:382-384(1994).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=21988050; PubMed=11991722; DOI=10.1006/geno.2002.6751; Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G., Korman K.; "A sequence-based map of the nine genes of the human interleukin-1 cluster."; Genomics 79:718-725(2002).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/dbrc.1999.1440; Mulero J.J., Pace A.M., Nelson S.T., Loeb D.D., Correa T.R., Dmanac R., Ford J.E.; "A novel interleukin-1 receptor antagonist gene"; Biochem. Biophys. Res. Commun. 263:702-706(1999).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=20092888; PubMed=10625660; DOI=10.1074/jbc.275.2.1169; Sims J.E., Renshaw B.R., Ketchum R.R., Kudin M., Garika K.E., "Four new members expand the interleukin-1 superfamily."; J. Biol. Chem. 275:1169-1175(2000).

RN [7]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308; Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tai-Singer R., Wells G.I., Doyle M.L., Young P.R.; "Identification and initial characterization of four novel members of the interleukin-1 family."; J. Biol. Chem. 275:10308-10314(2000).

RN [8]

RP SEQUENCE FROM N.A.

RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184; Busfield S.J., Comrack C.A., Yu G., Chikering T.W., Smutko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.; "Identification and gene organization of three novel members of the IL-1 family on human chromosome 2."; Genomics 66:213-216(2000).

RN [9]

RP SEQUENCE FROM N.A.

RX MEDLINE=21065532; PubMed=11145836; DOI=10.1006/cyto.2000.0799; Pan G., Riser P., Mo W., Baldwin D.T., Zhong A.W., Flvayoff B., Yansura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.; "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-1Rrp."; Cytokine 13:1-7(2001).

RN [10]

RP SEQUENCE FROM N.A.

RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200; Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussel J., Face A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.; "Cloning and characterization of IL-1HY2, a novel interleukin-1 family member."; J. Biol. Chem. 276:20597-20602(2001).

RN [11]

RP SEQUENCE FROM N.A.

RX MEDLINE=21359532; PubMed=11466363; Debetts R., Timane J.C., Homey B., Zurawski S., Sana T.R., Lo S., Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F., Kastelein R.A.; "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function as an antagonist and agonist of NF-kB activation through the orphan IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";

RT J. Immunol. 167:1440-1446(2001).

RN [12]

RP SEQUENCE FROM N.A.

RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3; Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J., Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G., Pan Y., Smith D.E., Young P.R.; "A new nomenclature for the IL-1-family genes"; Trends Immunol. 22:536-537(2001).

RT Trends Immunol. 22:536-537(2001).

CC -1- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DBJ third party annotation (TFA) entry.

CC -1- SIMILARITY: Belongs to the IL-1 family.

DR EMBL; BN000002; CAD29877.1; -.

DR HSSP; GQOY1; IM06.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005152; P:interleukin-1 receptor antagonist activity; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR GO; GO:0006954; P:inflammatory response; IEA.

DR InterPro; IPR008996; Cytok IL1 like.

DR InterPro; IPR003296; InterleukinIL1B.

DR InterPro; IPR003297; InterleukinIL1RA.

DR InterPro; IPR000975; Interleukin_1.

DR Pfam; PF00340; IL1; 1.

DR PRINTS; PR00264; INTERLEUKIN1.

DR PRINTS; PR01359; INTERLEUKIN1B.

DR PRINTS; PR01360; INTERLEUKIN1X.

DR ProDom; PD002536; Interleukin_1; 1.

DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN 1.

SQ SEQUENCE 155 AA; 16962 MW; B96DB58FA2612E25 CRC64;

Alignment Scores:

Pred. No.:	1.38e-08	Length:	155
Score:	174.50	Matches:	54
Percent Similarity:	42.60%	Conservative:	18
Best Local Similarity:	31.95%	Mismatches:	48
Query Match:	15.39%	Indels:	49
DB:	2	Gaps:	7

US-09-869-566-4 (1-650) x Q7RTZ6 (1-155)

RA Strausberg R.L., Fellnag E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stajich E.L., Martin J.A., Rubin G.M., Hong L.,
RA Stajich M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rata S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Maller J.A., Gnatatne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodegriem E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalish D.E., Scherch A., Schein J.E.,
RA Jones W.S., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the IL-1 family.
DR EMBL: BC042532; AAH42532.1; -.
DR HSSP: P18510; IILR.
DR MGD: MGI:96547; IILrn.
DR GO: GO:0030073; P:Insulin secretion; IMP.
DR GO: GO:0006629; P:lipid metabolism; IMP.
DR InterPro: IPR008996; CytoK IL1 like.
DR InterPro: IPR003297; InterleukinIL1RA.
DR InterPro: IPR009975; Interleukin_1.
DR Pfam: PF00340; IL1_1.
DR PRINTS: PRO0264; INTERLEUKIN1.
DR PRINTS: PRO1360; INTERLEUKIN1X.
DR ProDom: PD002536; Interleukin_1_1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Receptor.
SQ SEQUENCE 159 AA; 17995 MW; BCA081C12903367 CRC64;

Alignment Scores:
Pred. No.: 1,96e-08 Length: 159
Score: 173.00 Matches: 53
Percent Similarity: 47.278 Conservative: 25
Best Local Similarity: 32.128 Mismatches: 75
Query Match: 15.264 Indels: 12
DB: 2 Gaps: 7

US-09-869-566-4 (1-650) x Q8CGA1 (1-159)

QY 88 GCGAATTCAGCTCTTTGACAGAGGTCGAAGGTGAAGAACTTAACCCGAGAAATTCAGC 147
|||:::|||||:::|||||
Db 2 AAlaserglualalacysarprrosergerglylsarprcyglymetglnalapharg 21
|||:::|||||:::|||||

QY 148 ATTCATGACCAAGATCAACAAGTACGTGCTCGAGACTGCGGAATTCATGACGTTCCA 207
|||:::|||||:::|||||
Db 22 lltfrpaprthrasimllythrherytheluaigadnaenglnleuileala----- 39
|||:::|||||:::|||||

QY 208 GATMAAACTACATACGCG--CCAGAGATCTCTTGATTAAGCTCATCTCTGAGCTCA 264
|||:::|||||:::|||||
Db 40 -----Glytyleuindnglyprfoasnlle-----lybleugluclylyleuapmet 55
|||:::|||||:::|||||

QY 265 GCCTTCGCGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAGGGAGATTTGTCTC 324
|||:::|||||:::|||||
Db 56 valproilapspreuhisler---ValPheleuglylilehlglyglylyleucyleu 74
|||:::|||||:::|||||

QY 325 TATCTGACCAAGATTAAGACAAAGTATCATCCCTTCAGCTGAAGAGAGAAAGT 384
|||:::|||||:::|||||
Db 75 setcylatalybserclylaphaprtle-----lybleugluclyluclylvalasnlle 92
|||:::|||||:::|||||

Qy	385	ATGAAGCTGGCTGCCCAAAAGAAATACAGACGCCGGCCCTTATCTTTATATAGGCTCAG	444
Db	93	ThraspLeuSerLysAsnLysGluLysLysPyrAspG--PheThrPheLeuIleAspSerGlu	111
Qy	445	GTGGAGCTCTCTGGAACATCATCTGGAGTCGGCGGCTGACCCCGAATGGTTCATTCGACCTCC	504
Db	112	LysGlyPProThrTrnSerPheGluSerIleAlaIleCysProGlyTrpPheLeuGlyTrnTr	131
Qy	505	TGCAATTGTAAATGAGCCCTGTTGGGGTGAACAGATTAATTTGAGAACAGAAACATTT--	561
Db	132	LeuGluAlaAspArgProValSerLeuThrAsnThrProGluGluProLeuIleValThr	151
Qy	562	GAATTTTCATTTTCAA	576
Db	152	LysPheTrpPheGln	156

RESULT 15

ID	11F6_MOUSE	STANDARD	PRT	160 AA.
AC	OSULA2			
DT	28-FEB-2003 (Rel. 41, Last sequence)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUN-2004 (Rel. 44, Last annotation update)			
DE	Interleukin-1 family member 6 (IL-1F6) (interleukin-1 epsilon) (IL-1 epsilon) (F111 epsilon) (interleukin-1 homolog 1) (IL-1H1).			
GN	Name=I11f6; Synonyms=F111e, I11e, I11h1;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=202093405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;			
RA	Kumar S., McConnell P.C., Lehr R., Tierney L., Tzimas M.N.,			
RA	Grissold D.E., Cappe E.A., Tal-Singer R., Wells G.I., Doyle M.L.,			
RA	Young P.R.;			
RT	"Identification and initial characterization of four novel members of			
RT	the interleukin-1 family."			
RL	J. Biol. Chem. 275:10308-10314 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21359532; PubMed=11466363;			
RA	Debetz R., Timans J.C., Honey B., Zurawski S., Sana T.R., Lo S.,			
RA	Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,			
RA	Kastelein R.A.;			
RT	"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function			
RT	as an antagonist and agonist of NF-kappa B activation through the			
RT	Orphan IL-1 receptor-related protein 2."			
RL	J. Immunol. 167:1440-1446 (2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Embryo;			
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nakao I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotobori T.,			
RA	Badrall R., Hill D.P., Bule C., Hume D.A., Quackenbush J.,			
RA	Schiraldi L.M., Kaplin A., Matcunda H., Batilov S., Beisel K.W.,			
RA	Blake J.A., Bratt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,			
RA	Galler E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Daisterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gueticchi S., Hirokawa N., Jackson I.J., Jarvis E.D.,			
RA	Kanai A., Kanaji H., Kawasawa Y., Kedzierski R.M., King B.L.,			
RA	Konagaya A., Kurouchin I.V., Lee Y., Lenhard B., Lyons P.A.,			
RA	Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,			
RA	Nagasawa T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,			
RA	Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramchandran S.,			
RA	Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,			
RA	Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,			
RA	Sultana R., Takenader Y., Taylor M.S., Teasdale R.D., Tomita M.,			
RA	Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,			
RA	Wilmig L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,			
RA	Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carrinini P., Hayatsu N.,			

Result No.	Score	Query Match	Length	DB	ID	Description
1	650	100.0	650	6	BD2635568	BD2635568 IL-1 re1a
2	528.2	81.3	1006	6	BD2635567	BD2635567 IL-1 re1a
3	517	79.5	760	6	BC020637	BC020637 Homo sapi
4	517	79.5	847	6	AX133934	AX133934 Sequence
5	517	79.5	847	6	BD014862	BD014862 Polypepti
6	517	79.5	855	6	AX133936	AX133936 Sequence
7	517	79.5	855	6	BD014863	BD014863 Polypepti
8	517	79.5	1104	6	BD017454	BD017454 Protein b
9	516.8	79.5	787	9	AF167368	AF167368 Homo sapi
10	516.8	79.5	793	9	AF200456	AF200456 Homo sapi
11	516.8	79.5	802	6	AR183757	AR183757 Sequence
12	516.8	79.5	817	9	AF251118	AF251118 Homo sapi
13	516.8	79.5	839	6	BD2635581	BD2635581 IL-1 re1a
14	516.8	79.5	1600	6	BD242667	BD242667 Interleuk
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16	516	79.4	579	6	CQ722802	CQ722802 Sequence
17	516	79.4	579	6	AF201882	AF201882 Homo sapi
18	515.2	79.3	657	6	AR454216	AR454216 Sequence
19	515.2	79.3	657	9	AF251119	AF251119 Homo sapi

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42	366.2	56.3	654	6	BD242670	Interleuk	BD242670
41	367.8	56.6	654	6	BD242670	Interleuk	BD242670
40	392.2	60.3	534	6	BD080411	Novel mol	BD080411
39	392.2	60.3	501	6	BD080411	Novel mol	BD080411
38	392.2	60.3	408	6	BD080412	Novel mol	BD080412
37	394	60.6	474	6	BD251976	IL-1 zeta	BD251976
36	394	60.6	474	6	BD251976	IL-1 zeta	BD251976
35	395.6	60.9	506	6	BD263578	IL-1 zeta	BD263578
34	395.6	60.9	506	6	BD263578	IL-1 zeta	BD263578
33	396.6	61.0	537	9	AF251120	Homo sapi	AF251120
32	397	61.1	989	9	BD080409	Novel mol	BD080409
31	493.8	76.0	561	6	BD263570	IL-1 zeta	BD263570
30	501.6	77.2	629	6	BD263570	IL-1 zeta	BD263570
29	505.8	77.8	754	6	AX092410	Sequence	AX092410
28	505.8	77.8	754	6	BD263569	IL-1 zeta	BD263569
27	510.4	78.5	1225	6	AR454215	Sequence	AR454215
26	513	78.9	637	6	BD242669	Interleuk	BD242669
25	513.6	79.0	630	6	AX048211	Sequence	AX048211
24	513.6	79.0	630	6	BD276577	EXTREMBL	BD276577
23	514	79.1	594	9	AY071840	Homo sapi	AY071840
22	514	79.1	594	9	BD251975	IL-1 zeta	BD251975
21	514.2	79.2	656	6	BD263577	IL-1 zeta	BD263577
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ALIGNMENTS

RESULT 1				
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LOCUS	BD263568	650 bp	DNA	linear
DEFINITION	IL-1 related polypeptides.			
ACCESSION	BD263568			
VERSION	BD263568.1	GI:33073336		
KEYWORDS	JP 200253122-A/2.			
SOURCE	synthetic construct			
ORGANISM	other sequences; artificial sequences.			
REFERENCE	1. (bases 1 to 650)			
AUTHORS	Goddard, A. and Pan, J.			
TITLE	IL-1 related polypeptides			
JOURNAL	Patent: JP 200253122-A 2 08-OCT-2002;			

COMMENT

PN	JP	200253122-A/2	
PD	08-OCT-2002		
PF	22-DEC-1999	JP	2000591186
PR	23-DEC-1998	US	60/113430, 22-JAN-1999 US 60/116843
13-APR-1999	US	60/129122	
PI	AUDREY GODDARD, JAMES PAN		
PC	CI21N15/09, C07K14/475, C07K16/18, CI21N1/15, CI21N1/19, CI21N1/21, CI21N5/10,		
PC	CI2P21/02, CI2P21/08, CI21N15/00, CI21N5/00		
CC	recombinant DNA		
FH	Key	Location/Qualifiers	
FT	source	1..650	
FEATURES	location/Qualifiers	/organism='Artificial Sequence',	
source	1..650		

ORIGIN

Query Match	100.0%	Score 650;	DB 6;	length 650;
Best Local Similarity	100.0%	Pred. No. 5.7e-181;		
Matches 650; Conservative	0;	Mismatches	0;	Gaps 0

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Db 1 TAATTACCATGTCTGCACCTTCGATCTCTGTTGGAGCTGCAGTTCGACATAC 60
Oy 61 AAAGCAGTACGACAGCTTGGCGCGGAAATTCAGCTCTTTGACAGAGTCCAAAGGTG 120
Db 61 AAAGCAGTACGACAGCTTGGCGCGGAAATTCAGCTCTTTGACAGAGTCCAAAGGTG 120
Oy 121 AAGAACTTAAACCCGAGAAATTCAGATTCAGACAGATCACAAGTACTGTCCTG 180
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Db 241 GCATTAGCCTCATCTTGGAGCTCAGCTCTGCGGAGAAAGAAAGTCCGATTCCTGCGG 300
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Db 361 CTTCAGCTGGAAGAGAGAAATCTGATGAAGCTGCTGCCCAAAAGAAATCAGACGCGG 420
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RESULT 2
BD263567 1006 bp DNA linear PART 17-JUL-2003
LOCUS BD263567
DEFINITION IL-1-related polypeptides.
ACCESSION BD263567.1 GI:33073335
VERSION JP 2002533122-A/1.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1006)
TITLE Goddard, A. and Pan, J.
JOURNAL Il-1 related polypeptides
Patient: JP 2002533122-A 1 08-OCT-2002;
GENENTECH INC
OS Homo sapiens (human)
PN JP 2002533122-A/1
PD 08-OCT-2002
PF 23-DEC-1999 JP 2000591188
PR 23-DEC-1998 US 60/113430, 22-JAN-1999 US 60/116843 PR
PI 13-APR-1999 US 60/129122
PC ADDRESS GODDARD, JAMES PAM
PC C12N5/09, C07K14/475, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12N15/00, C12N5/00
CC Il-1 related polypeptides
FH Location/Qualifiers
FT source 1..1006
FT /organism='Homo sapiens (human)'.

FEATURES
source
Location/Qualifiers
1..1006
/organism="Homo sapiens"
/mol_type="Genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 81.3%; Score 528.2; DB 6; Length 1006;
Best Local Similarity 99.4%; Pred. No. 6,8e-145;
Matches 530; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 94 TCAGCTCTTTGACAGGTCGCAAGGTGAAGACTTAAACCCGAGAAATTCAGATTCAT 153
Db 409 TGAAGCTCTTTGACAGGTCGCAAGGTGAAGACTTAAACCCGAGAAATTCAGATTCAT 468
Oy 154 GACGAGATCACAAAAGTACTGCTGAGCTCTGGAATCTCATAGCAGTTCCAGATTA 213
Db 469 GACGAGATCACAAAAGTACTGCTGAGCTCTGGAATCTCATAGCAGTTCCAGATTA 528
Oy 214 AACTACATAGCCCGAGAGATCTTTTGCAATAGCTCATCTTGAAGCTCAGCTCTGCG 273
Db 529 AACTACATAGCCCGAGAGATCTTTTGCAATAGCTCATCTTGAAGCTCAGCTCTGCG 588
Oy 274 GAGAAAGGAAGTCCGATTTCTCTGGGGCTCTTAAGGGAGATTTCCTCACTGATAC 333
Db 589 GAGAAAGGAAGTCCGATTTCTCTGGGGCTCTTAAGGGAGATTTCCTCACTGATAC 648
Oy 334 AAGATTAAGGACAAAGTCAATCATCTTCACTGAGCTGAAGAGAGAAATGAGAGCTG 393
Db 649 AAGATTAAGGACAAAGTCAATCATCTTCACTGAGCTGAAGAGAGAAATGAGAGCTG 708
Oy 394 GCTGCCCAAAAGGATGACAGCGCGGCTTTCATCTTTATAGGGCTCAGGTGGGCTCC 453
Db 709 GCTGCCCAAAAGGATGACAGCGCGGCTTTCATCTTTATAGGGCTCAGGTGGGCTCC 768
Oy 454 TGGAAATGCTGAGATCGCGGGCTCACCGCGAGTGTTCATCTGACCTCTGCAATTGT 828
Db 769 TGGAAATGCTGAGATCGCGGGCTCACCGCGAGTGTTCATCTGACCTCTGCAATTGT 828
Oy 514 AATGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTT 573
Db 829 AATGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTT 888
Oy 574 CAACCAATTTGCAAGCTGAATATGAGCCCGAGTGAAGTCAAGGATTAAGGATAC 626
Db 889 CAACCAATTTGCAAGCTGAATATGAGCCCGAGTGAAGTCAAGGATTAAGGATAC 941

RESULT 3
BC020637 760 bp mRNA linear PRI 29-JUN-2004
LOCUS BC020637
DEFINITION Homo sapiens interleukin 1 family, member 7 (zet), transcript variant 1, mRNA (cDNA clone MGC:22276 IMAGE:473123), complete cds.
ACCESSION BC020637.1 GI:18088327
VERSION MGC.
KEYWORDS
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 760)
TITLE Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, S., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Utsidi, T.B., Toshilyak, S., Carrinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McWhan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.W., Gay, L.J., Hult, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Patel, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED
12477932

REFERENCE
2 (bases 1 to 760)
Strausberg, R.
Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mdc@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

REMARK
COMMENT
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
Series: ITAL Plate: 37 Row: h Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894299.
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ORIGIN
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Best Local Similarity 97.2%; Pred. No. 1.4e-141;
Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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626 C 626
665 C 665

RESULT 4
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LOCUS AX133934
DEFINITION Sequence 4 from Patent EP1092773.
ACCESSION AX133934
VERSION AX133934.1 GI:14139876
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Ushio, S., Nukada, Y., Yamamoto, K. and Kurimoto, M.
TITLE Polypeptide and uses thereof
JOURNAL Patent: EP 1092773-A 4 18-APR-2001;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
FEATURES
Location/Qualifiers
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Query Match 79.5%; Score 517; DB 6; Length 847;
Best Local Similarity 97.2%; Pred. No. 1.4e-141;
Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Best Local Similarity	97.2%;	Pred. No. 1.4e-141;		

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ORIGIN

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 Best Local Similarity 97.2%; Pred. No. 1,4e-141;
 Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 782 C 782

RESULT 7
 BD014863 855 bp DNA linear PAT 27-AUG-2002
 LOCUS Polypeptide and utilization thereof.
 ACCESSION BD014863
 VERSION BD014863.1 GI:22555670
 KEYWORDS JP 2001178479-A/5.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 855)
 Uehio, S., Nukata, Y., Yamamoto, K. and Kurimono, M.
 Polypeptide and utilization thereof
 Patent: JP 2001178479-A 5 03-JUL-2001;
 HAYASHIBARA BIOCHEMICAL LABORATORIES INC DIRECTOR GENERAL OF
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND
 OS Homo sapiens (human)
 PN JP 2001178479-A/5
 PD 03-JUL-2001
 PF 13-OCT-2000 JP 2000312761
 PI SHINBEI USHIO,YOSHITUKI NUKATA,KOZO YAMAMOTO,MASASHI KURIMOTO
 PC C12N15/09,A61K38/00,A61K39/395,A61P37/00,A61P43/00,
 PC C07K14/545,
 PC C07K14/715,C07K16/24,C12N1/21,C12P21/02,C12P21/02//C12P21/08,

PC (C12P21/02,C12R1:19), (C12P21/02,C12R1:91), C12N15/00,A61K37/02
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 FH Key Location/Qualifiers
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ORIGIN

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 Best Local Similarity 97.2%; Pred. No. 1,4e-141;
 Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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 ACCESSION BD017454
 VERSION BD017454.1 GI:22558630
 KEYWORDS JP 2001231578-A/2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1104)
 Matsushita, T., Sakakibara, T., Sekine, S., Sato, M., Sakurai, S. and
 Furuya, A.
 Protein belonging to IL-1family
 Patent: JP 2001231578-A 2 28-AUG-2001;
 KYOMA HAKKO KOGYO CO LTD

COMMENT OS Homo sapiens (human)
PN JP 2001231578-A/2
PD 28-AUG-2001
PF 07-DEC-2000 JP 2000372864
PI TAKESHI MATSUSHITA, TOSHIHIRO SAKAKIBARA, SUSUMU SEKINE, MITSUO
PI SATO
PI SATOU SAKURAI, AKIRO FURUYA
PC C12N15/09, A01K67/027, A61K31/711, A61K38/00, A61K39/395, A61K39/
PC 395, A61K48/00,
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A61P1/04, A61P5/48, A61P5/50, A61P9/10, A61P11/06, A61P19/08, A61P19/ PC
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PC A61P43/00,
PC C07K14/545, C07K16/24, C12N1/15, C12N1/19, C12N1/21, C12N5/10, PC
C12P21/02,
PC C12P21/08, C12Q1/68, G01N33/53, G01N33/577//C12N5/10, C12R1:91),
PC C12N15/00,
PC A61K37/02, C12N5/00, (C12N5/00, C12R1:91)
CC Protein belonging to IL-1family
FH Key location/Qualifiers
FT CDS (370)..(1023).
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Best Local Similarity 97.2%; Pred. No. 1.4e-141;
Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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626 C 626

Db 1031 C 1031
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AF167368
LOCUS Homo sapiens IL-1x protein mRNA, complete cds.
DEFINITION
ACCESSION AF167368
VERSION AF167368.1 GI:11093527
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Manolj, P.P., Mancovani, A. and Muzio, M.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-1999) Immunology, IRFM Mario Negri, Via-Bricrea;
62, Milano 20157, Italy
FEATURES
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ORIGIN
Query Match 79.5%; Score 516.8; DB 9; Length 787;
Best Local Similarity 98.7%; Pred. No. 1.6e-141;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
99 TCTTTGCAAGGTCCTCAAGGTAAGACTTAACCCGAGAAATTCAGATTCATGACCA 158
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Qy 579 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGTAC 626
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RESULT 10
AF200496 793 bp mRNA linear PRI 11-MAY-2000
LOCUS Homo sapiens interleukin-1 homolog 4 mRNA, complete cds.
DEFINITION AF200496
ACCESSION AF200496.1 GI:7769119
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 793)
Kumar,S., McDonnell,P.C., Lehr,R., Tierney,L., Tzimas,M.N.,
Griswold,D.E., Capper,E.A., Tai-Singer,R., Wells,G.I., Doyle,M.L.
and Young,P.R.
TITLE Identification and initial characterization of four novel members
of the interleukin-1 family
JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)
MEDLINE 20209405
PUBMED 10744718
REFERENCE 2 (bases 1 to 793)
Kumar,S., McDonnell,P.C. and Young,P.R.
TITLE Direct Submission
AUTHORS Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA
FEATURES
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Query Match 79.5%; Score 516.8; DB 9; Length 793;
Best Local Similarity 98.7%; Pred. No.1.6e-141;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 159 GGATCACAAGATGATCTGTCCTGAGTCTGGGAATTCATAGAGTTCAGATTAATAACTA 218
Db 243 GGATCACAAGATGATCTGTCCTGAGTCTGGGAATTCATAGAGTTCAGATTAATAACTA 302

Qy 219 CATAGCCCAAGATCTCTTTCGATTAAGCTCATCTTGAAGTCAAGCTTCGCGAGAA 278
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Qy 399 CCAAAAGGATGACACGCGCGCCCTTCATCTTTTATAGGGCTCAAGTGGCTCTCGAA 458
Db 483 CCAAAAGGATGACACGCGCGCCCTTCATCTTTTATAGGGCTCAAGTGGCTCTCGAA 542

Qy 459 CATGCTGAGTGGGGGCTCACCCGGATGTTGATCTGACCTCTGCAATTTGATGA 518
Db 543 CATGCTGAGTGGGGGCTCACCCGGATGTTGATCTGACCTCTGCAATTTGATGA 602

Qy 519 GCTGTGGGGTGAAGATTAATTTGAGAAACAGAAACATTTGATTTTCAATTCACC 578
Db 603 GCTGTGGGGTGAAGATTAATTTGAGAAACAGAAACATTTGATTTTCAATTCACC 662

Qy 579 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGTAC 626
Db 663 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAAGGAAC 710

RESULT 11
AR183757 802 bp DNA linear PAT 20-APR-2002
LOCUS AR183757
DEFINITION Sequence 1 from patent US 6342371.
ACCESSION AR183757
VERSION AR183757.1 GI:20227726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 802)
McDonnell,P.C. and Young,P.R.
TITLE Interleukin-1 homologue, IL-1H4
JOURNAL Patent: US 6342371-A 1 29-JAN-2002;
FEATURES
source Location/Qualifiers
1..802
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 79.5%; Score 516.8; DB 6; Length 802;
Best Local Similarity 98.7%; Pred. No.1.6e-141;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 99 TCTTTCGAGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGATTATGACCA 158
Db 192 TGTTCACACAAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGATTATGACCA 251

Qy 159 GGATCACAAGATGATCTGTCCTGAGTCTGGGAATTCATAGAGTTCAGATTAATAACTA 218
Db 252 GGATCACAAGATGATCTGTCCTGAGTCTGGGAATTCATAGAGTTCAGATTAATAACTA 311

Qy 219 CATAGCCCAAGATCTCTTTCGATTAAGCTCATCTTGAAGTCAAGCTTCGCGAGAA 278
Db 312 CATAGCCCAAGATCTCTTTCGATTAAGCTCATCTTGAAGTCAAGCTTCGCGAGAA 371

Qy 279 AGGAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGA 338
Db 372 AGGAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGACAGA 431

Qy 339 TAAAGACAAAGTCAATCCATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTGGCTC 398
Db 432 TAAAGACAAAGTCAATCCATCCCTTCAGCTGAAGAGAAAGAACTGATGAAGCTGGCTC 491

Qy 399 CCAAAAGGATGACACGCGCGCCCTTCATCTTTTATAGGGCTCAAGTGGCTCTCGAA 458
Db 492 CCAAAAGGATGACACGCGCGCCCTTCATCTTTTATAGGGCTCAAGTGGCTCTCGAA 551

Qy 459 CATGCTGAGTGGGGGCTCACCCGGATGTTGATCTGACCTCTGCAATTTGATGA 518
Db 552 CATGCTGAGTGGGGGCTCACCCGGATGTTGATCTGACCTCTGCAATTTGATGA 611

Db	Qy	RESULT 12
519	GCCTGTTGGGGGACAGATTAATTTAGAAACAGGAAACACATTGAAATTTTCATTTCACAC	578
612	GCTGTTGGGGGTGACAGATTAATTTAGAAACAGGAAACACATTGAAATTTTCATTTCACAC	671
579	AGTTTGCAGAGCTGAATAGCCCCAGTAGGTCAGCGATTAGGATAC	626
672	AGTTTGCAGAGCTGAATAGCCCCAGTAGGTCAGCGATTAGGAAAC	719
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LOCUS	Homo sapiens interleukin-1-related protein long isoform a mRNA,	
DEFINITION	complete cds; alternatively spliced.	
ACCESSION	AF251118	
VERSION	AF251118.1 GI:10185735	
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 817)	
JOURNAL	Pan,G., Risseer,P., Mao,W., Baldwin,D.T., Zhong,A.W., Filvaroff,E.,	
MEDLINE	Yasunura,D., Lewis,L., Bisenberg,C., Henzel,W.J. and Vandenberg,R.	
PUBMED	IL-1H, an interleukin 1-related protein that binds IL-18	
REFERENCE	receptor/IL-1Rrp	
AUTHORS	Cytokine 13 (1), 1-7 (2001)	
TITLE	2 (bases 1 to 817)	
JOURNAL	Pan,G., Baldwin,D.T. and Zhong,A.W.	
MEDLINE	Direct Submission	
PUBMED	Submitted (03-Apr-2000) Endocrinology, Genentech, Inc., 1 DNA Way,	
REFERENCE	South San Francisco, CA 94080, USA	
AUTHORS	Location/Qualifiers	
TITLE	1..817	
JOURNAL	/organism="Homo sapiens"	
MEDLINE	/mol_type="mRNA"	
PUBMED	/db_xref="taxon:9606"	
REFERENCE	73..729	
AUTHORS	/note="IL-1H; IL-1 family member; binds IL-18	
TITLE	receptor/IL-1Rrp; putative involvement in inflammation and	
JOURNAL	immune responses"	
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AUTHORS	/db_xref="GI:10185735"	
TITLE	/translation="MSFVGENSGVMSGEDEKDEPOCLEDPPAGSPLEPSPS/PTMNM	
JOURNAL	FVHSPRYKYNLNPKKSFILHDDHXYLVISDNILAVDPKXVIREIPFALASISLSSAS	
MEDLINE	AEKSPILGVTSKGEFCLCYDRDKQSHSPSIQLKEKLMKLAQKESARRPFITRRAC	
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REFERENCE	"	
ORIGIN		
Query Match	79.5%; Score 516.8; DB 9; Length 817;	
Best Local Similarity	98.7%; Pred. No. 1.6e-14;	
Matches	521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Qy	99 TCTTTGCAGAGGTCAAGGAGGAGAACCTTAAACCCGAGAAATTCAGCATTCATGACCA	158
Db	207 TGTTCACCAAGTCCAAAGGTGAGAACTTAAACCCGAGAAATTCAGCATTCATGACCA	266
Qy	159 GGATCACAAGATCTGTCTGTGACTCTGGATCTCATAGCAGTTCCAGATTAATAACTA	218
Db	267 GGATCACAAGATCTGTCTGTGACTCTGGATCTCATAGCAGTTCCAGATTAATAACTA	326
Qy	219 CATACGCCCAAGATCTTTTGCATTAGCTCATCTTGAAGCTAGAGCTCTGGGAGAA	278
Db	327 CATACGCCCAAGATCTTTTGCATTAGCTCATCTTGAAGCTAGAGCTCTGGGAGAA	386
Qy	279 AGGAAGTCCGATTCCTCGGGGGTCTTAAAGGGGAGTTTGTCTTACTGACCAAGAA	338
Db	387 AGGAAGTCCGATTCCTCGGGGGTCTTAAAGGGGAGTTTGTCTTACTGACCAAGAA	446

OY	339	TAAAGACAAGAGTATCATCATTCTTTGACGTGAAGAAGAAACTGATGAAGCTGGCTGC	398
Db	447	TAAAGACAAGAGTATCATCATTCTTTGACGTGAAGAAGAAACTGATGAAGCTGGCTGC	506
OY	399	CCAAAAGAAATCAGCACGCCCGGCTTCATCTTTTAATAGGGCTCAGGTGGGCTCTTGAA	458
Db	507	CCAAAAGAAATCAGCACGCCCGGCTTCATCTTTTAATAGGGCTCAGGTGGGCTCTTGAA	566
OY	459	CATCTGTGAGTCGGCGGGCTCACCCCGATGGTTATCTGCACCCTCGCAATTGTATGA	518
Db	567	CATCTGTGAGTCGGCGGGCTCACCCCGATGGTTATCTGCACCCTCGCAATTGTATGA	626
OY	519	GCCGTGGGGGTGACATAATAATTGAGAACAGAAAACACTGAATTTTCATTTC AAC	578
Db	627	GCCGTGGGGGTGACATAATAATTGAGAACAGAAAACACTGAATTTTCATTTC AAC	686
OY	579	AGTTTGCAAAGCTGAAATGAGCCCCAGTAGGTGACGATTAAGGATAC	626
Db	687	AGTTTGCAAAGCTGAAATGAGCCCCAGTAGGTGACGATTAAGGATAC	734
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LOCUS	BD263581	839 bp	DNA linear PAT 17-JUL-2003
DEFINITION	IL-1 related polypeptides.		
ACCESSION	BD263581		
VERSION	BD263581.1 GI:33073349		
KEYWORDS	JP 2002533122-A/15.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	Goddard,A. and Pan,J. IL-1 related polypeptides Patent: JP 2002533122-A 15 08-OCT-2002;		
AUTHORS	JOURNAL		
COMMENT	GENENTECH INC OS Homo sapiens (human) PN JP 2002533122-A/15 PD 08-OCT-2002 PR 22-DEC-1999 JP 2000591188 PR 23-DEC-1998 US 60/113430.22-JAN-1999 US 60/116843 PR PI AUDREY GODDARD,JAMES PAN PC C12N15/09,C07K14/475,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC C12N5/10, PC C12P21/02,C12P21/08,C12N15/00,C12N5/00 CC IL-1 related polypeptides FH key Location/Qualifiers FT Source 1..839 FT /organism='Homo sapiens (human)'. location/Qualifiers 1..839 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
FEATURES	source		
ORIGIN			
Query Match	79.5%; Score 516.8; DB 6; Length 839;		
Best Local Similarity	98.7%; Pred.No.1.6e-141;		
Matches 521; Conservative	0; Mismatches 7; Indels 0; Gaps 0;		
OY	99	TCTTTGAGAGGTCCAAAGGTGAAGAACTTAAACCCGAAAGAAATTCAGATTCATGACCA	158
Db	207	TGTTTCACAAAGTCCAAAGGTGAAGAACTTAAACCCGAAAGAAATTCAGATTCATGACCA	266
OY	159	GGATCACAAAGTACTGCTCTGGA CTCTGGGAATTCATAGCAGTTCAGATAAAAACTA	218
Db	267	GGATCACAAAGTACTGCTCTGGA CTCTGGGAATTCATAGCAGTTCAGATAAAAACTA	326
OY	219	CATACGCCAGAGATCTTTTGATTAAGCCTATCTTGAGCTCAGGCTCTGGGGAGAA	278

Db 327 CATAGCCGAGAGATCTTTTGATTAGCTCATCTTGAAGTCAAGCTCTGCGGAGAA 386
Oy 279 AGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 338
Db 387 AGGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 446
Oy 339 TAAAGACAAAGTCAATCCATCCCTTCACTGAGAGAGAAAGTATGATGAGCTGCTC 398
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Oy 399 CCAAAAGGATGACAGACGCGCGGCTTCACTTTATAGGGCTCAGTGGGCTCTCGAA 458
Db 507 CCAAAAGGATGACAGACGCGCGGCTTCACTTTATAGGGCTCAGTGGGCTCTCGAA 566
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Db 567 CATGCTGAGTGGGGGCTCAAGCTGATGATGATGATGATGATGATGATGATGATGAT 626
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Db 627 GCCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCAATTTCAAC 686
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RESULT 14
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LOCUS Interleukin-1 homolog ZIL1A4.
DEFINITION BD242667
ACCESSION BD242667.1 GI:33052437
VERSION JP 2002528079-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1600)
Interleukin-1 homolog ZIL1A4
Patent: JP 2002528079-A 1 03-SEP-2002;
ZYMOGENETICS INC
COMMENT OS Homo sapiens (human)
PN JP 2002528079-A/1
PD 03-SEP-2002
PF 27-OCT-1999 JP 2000578451
PR 27-OCT-1998 US 09/179614
PI ROBERT R WEST, PAUL O SHEPPARD, ZEREN GAO
PC C12N15/09, A61K38/00, A61P37/02, C07K14/545, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12N15/00, C12N5/00, A61K37/02 CC
Interleukin-1 homolog ZIL1A4
FH Key Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Query Match 79.5%; Score 516.8; DB 6; Length 1600;
Best Local Similarity 98.7%; Pred. No. 1.7e-141;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 219 CATAGCCGAGAGATCTTTTGATTAGCTCATCTTGAAGTCAAGCTCTGCGGAGAA 278
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Oy 279 AGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 338
Db 1161 AGGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 1220
Oy 339 TAAAGACAAAGTCAATCCATCCCTTCACTGAGAGAGAAAGTATGATGAGCTGCTC 398
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Oy 399 CCAAAAGGATGACAGACGCGCGGCTTCACTTTATAGGGCTCAGTGGGCTCTCGAA 458
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Db 1401 GCCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCAATTTCAAC 1460
Oy 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCTTGAAGGTAC 626
Db 1461 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCTTGAAGGTAC 1508

RESULT 15
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LOCUS IL-1 zeta, IL-1 zeta splice variants and Xrec2 DNAs and
DEFINITION BD251972
ACCESSION BD251972.1 GI:33061742
VERSION JP 2002532094-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 579)
IL-1 zeta, IL-1 zeta splice variants and Xrec2 DNAs and
polypeptides
Patent: JP 2002532094-A 1 02-OCT-2002;
IMMUNEX CORP
COMMENT OS Homo sapiens (human)
PN JP 2002532094-A/1
PD 02-OCT-2002
PF 14-DEC-1999 JP 2000588357
PR 14-DEC-1998 US 60/112163, 10-NOV-1999 US 60/164675 PI
JOHN E SIMS, DIRK E SMITH, TERESA L BORN
PC C12N15/09, C07K14/47, C07K14/715, C07K16/24, C07K16/28, C12N1/15,
PC C12N1/19, C12N5/10, C12P21/02, C12P21/08, C12N15/00, C12N5/00 CC
IL-1 zeta, IL-1 zeta splice variants and Xrec2 DNAs and
polypeptides
FH Key Location/Qualifiers
FT source 1..579
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.7e-141;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 64 AGAGTCCAAAGTGAAGACTTAACCCGAAATTCAGATTCAATGACCGAGATCAC 123
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OY 166 AAAGTACGAGTCTCGGATCTCGGATCTCATAGCAGTTCCAGATAAAACTACATACGC 225
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Db 124 AAAGTACGAGTCTCGGATCTCGGATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
    |||||
OY 226 CCAGAGATCTTCTTGCAATTAGCTCATCTTGAGCTCAGCTCTGCGAGAAAGAAAGT 285
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Db 184 CCAGAGATCTTCTTGCAATTAGCTCATCTTGAGCTCAGCTCTGCGAGAAAGAAAGT 243
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OY 286 CCGATTCTCTGGGGGCTCTTAAGGGAGTTTGTCTACTGTGACAAGATTAAGGA 345
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Db 244 CCGATTCTCTGGGGGCTCTTAAGGGAGTTTGTCTACTGTGACAAGATTAAGGA 303
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OY 346 CAAAGTCAATCCATCCCTTCAGCTGAAGAAAGAAAGTGAAGCTGGCTGCCAAAG 405
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Db 304 CAAAGTCAATCCATCCCTTCAGCTGAAGAAAGAAAGTGAAGCTGGCTGCCAAAG 363
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OY 406 GAATCAGCAGCCGCGCCCTTCATCTTTATAGGGCTCAGTGGCTCCTGAAACATGCTG 465
    |||||
Db 364 GAATCAGCAGCCGCGCCCTTCATCTTTATAGGGCTCAGTGGCTCCTGAAACATGCTG 423
    |||||
OY 466 GAGTGGCGGCTCAACCCGAGATGTTCACTGCACTCTGCAATTGTAATGAGCTGTT 525
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Db 424 GAGTGGCGGCTCAACCCGAGATGTTCACTGCACTCTGCAATTGTAATGAGCTGTT 483
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OY 526 GGGGTGACAGATAATTGTAAGAACAGAAACATTTGATTTCAACCAAGTTGC 585
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Db 484 GGGGTGACAGATAATTGTAAGAACAGAAACATTTGATTTCAACCAAGTTGC 543
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OY 586 AAAGCTGAATAGCCCAAGTGAAGTCAAGCGATTAG 621
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Db 544 AAAGCTGAATAGCCCAAGTGAAGTCAAGCGATTAG 579
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Search completed: May 28, 2005, 16:28:51
Job time : 3012 secs

XX
PI Goddard A, Pan J;
XX
DR MPI: 2000-452395/39.
XX
DR P-PSDB; AAY96933.
XX

PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis.
XX

XX Claim 7, Fig 2; 143pp; English.

XX An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1 β) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (IL-1RAc) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1 β polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of an active peptide). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1 β protein expression and activity which may be used to
CC treat disorders associated with inappropriate IL-1 β expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease
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XX Sequence 650 BP; 176 A; 156 C; 162 G; 156 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 650; DB 3; Length 650;
XX Best Local Similarity 100.0%; Pred No. 5.3e-203;

XX Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 TAAATCAGCATGCTGCACTTCTGATCTAGCTCTTGTGAGCTCAGTCTGACTAC 60
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XX 61 AAAGAGATGACGACAAAGCTTGGCGCGGAATTCAGCTCTTGGCAGAGTCCAAAGGTG 120
DB 61 AAAGAGATGACGACAAAGCTTGGCGCGGAATTCAGCTCTTGGCAGAGTCCAAAGGTG 120
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XX 121 AAGAATCTTAAACCGAAGAAATCAGATTCATGACAGAGATCAAAAGTACTGCTCTG 180
DB 121 AAGAATCTTAAACCGAAGAAATCAGATTCATGACAGAGATCAAAAGTACTGCTCTG 180
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XX 181 GACTCTGGGATCTCATAGCAGTTCAGATTAATAAATCACTAGCCCAAGATCTTCTT 240
DB 181 GACTCTGGGATCTCATAGCAGTTCAGATTAATAAATCACTAGCCCAAGATCTTCTT 240
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XX
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DB 241 GCATTAGCTCATCTTGAAGCTCAGCTTCGCGAAGAAAGAGTTCGATCTCTCGGG 300
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DB 301 GTCTCTAAGGGAGTGTCTCTCTACTGACAGAGATTAAGGAAAGATCATTCATCC 360
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DB 361 CTTCAAGTGAAGAGAAATGATGAGTGGTCCCAAAAGGATCAGACGCGG 420
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DB 421 CCCTTCATCTTTAAGGGCTCAGGTGGGCTCTGGAACATGCTGAGTGGCGGCTCAC 480
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XX 481 CCGGAGATGTTCAATGCACTCTCTGCAATTTGAATAGCTGTGGGGGACAGATTA 540
DB 481 CCGGAGATGTTCAATGCACTCTCTGCAATTTGAATAGCTGTGGGGGACAGATTA 540
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XX 541 TTGAGAAACAGAAACACATTTGATTTTCACTTCAACCAAGTTGCAAGCTGAATAGC 600

DB 541 TTGAGAAACAGAAACACATTTGATTTTCACTTCAACCAAGTTGCAAGCTGAATAGC 600
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XX 601 CCAGTGAAGTCAAGGATTTAGAGTACAGTCACTTAGAGATCCCGG 650
DB 601 CCAGTGAAGTCAAGGATTTAGAGTACAGTCACTTAGAGATCCCGG 650

RESULT 2
AAAS1591
ID AAAS1591 standard; DNA; 1006 BP.

XX AAAS1591;

XX 31-OCT-2000 (first entry)

XX Human IL-1 receptor antagonist 1 related DNA.

XX hIL-1RAc; human interleukin-1 receptor antagonist-1; IL-1 β ; osteopathic;

XX interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;

XX anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;

XX dermatological; immunomodulatory; gastrointestinal; gene therapy; ds.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

XX CDS 103..936

XX /tag= a

XX exon 103..180

XX /tag= b

XX intron 180..432

XX /tag= c

XX exon 433..933

XX /tag= d

XX WO200039297-A2.

XX 06-JUL-2000.

XX 22-DEC-1999; 99WO-US030720.

XX 23-DEC-1998; 98US-0113430P.

XX 22-JAN-1999; 99US-011643P.

XX 13-APR-1999; 99US-0129122P.

XX (GETH) GENENTECH INC.

XX Goddard A, Pan J;

XX MPI: 2000-452395/39.

XX P-PSDB; AAY96931, AAY96932.

XX Nucleic acids encoding interleukin-1-like polypeptides, useful for

XX preventing and treating e.g. inflammation, asthma and psoriasis.

XX Example 1; Fig 1A-B; 143pp; English.

XX An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1 β) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (IL-1RAc) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1 β polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of an active peptide). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1 β protein expression and activity which may be used to
CC treat disorders associated with inappropriate IL-1 β expression and
CC activity, such as inflammatory disorders, asthma, arthritis, adult
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress

CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC periarthritis, graft versus host disease and/or inflammatory bowel disease
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SQ Sequence 1006 BP; 289 A; 246 C; 241 G; 230 T; 0 U; 0 Other;

Query March	81.3%	Score 528.2	DB 3	Length 1006
Best Local Similarity	99.4%	Pred. NO. 8.9e-163		
Matches 530	Conservative 0	Mismatches 3	Indels 0	Gaps 0

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Qy		94	TGACCTTTTTCAGAGGTCCAAAGTGAAACTTAACCAGAATAATTCAGATTCAAT	153
Db		154	GACCAGATCATCAAAGTACTGGTCTCTGSACTCTCGGAATCTCATAGCAGTTCCAATAAA	213
Qy		469	GACCAGATCATCAAAGTACTGGTCTCTGSACTCTCGGAATCTCATAGCAGTTCCAATAAA	528
Db		214	AACATCAATAGCCCCAGAGATCTCTCTTTGCATTAGGCTATCCTTAGCTCACCTCTGGG	273
Qy		529	AACATCAATAGCCCCAGAGATCTCTCTTTGCATTAGGCTATCCTTAGCTCACCTCTGGG	588
Db		274	GAGAAAGGAAGTCCGATTCTCTCGGGGCTCTCTAAGGGGAGTTTGTCTCTACGTGAC	333
Qy		589	GAGAAAGGAAGTCCGATTCTCTCTCGGGGCTCTCTAAGGGGAGTTTGTCTCTACGTGAC	648

[illegible]

RESULT 3
AAC85680
ID AAC85680 standard; cDNA; 847 BP.

DT 29-JUN-2001 (first entry)

CDNA encoding IL-1 related substance.

KM Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;
KM natural killer activity; immune system; gene therapy; immunodeficiency;
KM 88.

Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	121. .777

PN EP1092773-A2

PD 18-APR-2001.

PF 11-OCT-2000; 2000EP-00308948.

PR 15-OCT-1999; 99JP-00294493.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU

PI Ushio S, Nukada Y, Yamamoto K, Kurimoto M

DR WPI; 2001-275206/29

DR P-PSDB; AAB47186

PT New human interleukin-1-related polypeptide and polynucleotide, useful
PT for gene therapy and in developing drugs as regulators of natural killer
PT activity, are capable of inhibiting natural killer activity.

PS Claim 4; Page 13; 15pp; English.

CC This sequence encodes an interleukin-1 (IL-1)-related polypeptide. IL-1
CC related polypeptide was isolated from Hsp-MT cells, FERM-BP-2430, an
CC established human T-cell line. IL-1-related polypeptide is useful for
CC inhibiting natural killer (NK) activity, which is related to the immune
CC system of mammals. The DNA encoding the IL-1 related polypeptide is
CC useful in gene therapy of patients in need of NK activity inhibition and
CC others suffering from immunodeficiency

SQ Sequence 847 BP; 244 A; 210 C; 202 G; 191 T; 0 U; 0 Other;

```
Query Match      79.5%: Score 517; DB 4; length 847;
Best Local Similarity 97.2%: Pred. No. 4e-159;
Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0
```

Dy 86 CCGGAAATTCAGCTTTCCAGAGGTCCAAGGTGAAGAATTAAACCGAAGAAATTC 145

Db 242 CCGCATGAATTTTGTCAACAAGTCCAAGGTGAAGAATTAAACCGAAGAAATTC 301

146 GCATTCAATGACAGATCA CAAAGTAAGTGGTCTGGAATCTCATATGACATTC 205
 302 GCATTCAATGACAGATCA CAAAGTAAGTGGTCTGGAATCTCATATGACATTC 361

Qy 206 CAGATAAAACTACATACGCCAGAGATCTTCTTGCAATTAGCCTCATCCTTGAGCTCAG 285

Db 362 CAGATAAAACTACATACGCCAGAGATCTTCTTGCAATTAGCCTCATCCTTGAGCTCAG 421

Dy 266 CCTCTGCGAGAAAGGAAGTCCGATTCTCTGGGGGTCTCAAAAGGGAGTTTTGTCTCT 325
|||||
Db 422 CCTCTGCGAGAAAGGAAGTCCGATTCTCTGGGGGTCTCAAAAGGGAGTTTTGTCTCT 481

Qy 326 ACTGTGACAGATPAAAGCAAAAGTCATCCCTTACGCTGAAGAGGAAACCTGA 3855

Db 482 ACTGTGACAGATPAAAGCAAAAGTCATCCCTTACGCTGAAGAGGAAACCTGA 5411

DY 386 TGAAGCTGGCTGCCAAAAGAAATCAGACGCCGCCCTTCATCTTTTATAGGGCTCAGG 445
|||||
D6 512 TGAAGCTGGCTGCCAAAAGAAATCAGACGCCGCCCTTCATCTTTTATAGGGCTCAGG 6010
|||||

DY 446 TGGGCTCCTGAACATGTCTGGAGTCCGCCGCTCACCCCGAATTGCATCTGCACCmCCT 505
| | | | |
Db 602 TGSSCTCTGGAACATGTCTGGAGTCGGCGGCTACCCCAGATGTCTGCATCTGCACmCCT 661

QY 506 GCAATTGTAATGAACCTGTGGGGTGCACATAAATTGAGAACAGAAACACTTGAT 565
|||||
|||

bB 662 GC AATTGTAATGAGCCTGTGGGGGACAGATAAATTGAGAACAGAAACACTTGAT 721
|||||

QY 566 TTTTCATTTTCAACCAAGTTTGGCAAGCTGAAATGAGCCCCAGTGGAGTTCAGCGCATTTAGGCTA 625
|||||
722 TTTTTCATTTTCAACCAAGTTTGGCAAGCTGAAATGAGCCCCAGTGGAGTTCAGCGCATTTAGGCTA 781
|||||

QY	626	C	626
Db	782	C	782

RESULT 4
AA171179
ID ,AA171179 standard; cDNA; 1104 BP

```

XX AA171179;
AC 22-JAN-2002 (first entry)
XX
XX Human interleukin 1 family protein encoding cDNA SEQ ID NO:4.
DE Human interleukin 1, IL-1; growth factor; Tango-77; diagnosis;
XX Human; interleukin 1, IL-1; growth factor; Tango-77; diagnosis;
KW identification; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 370..1026
FT CDS /*tag= a
FT /product= "IL-1 family protein"
FT
XX JP2001231578-A.
XX
XX 28-AUG-2001.
XX
XX 07-DEC-2000; 2000JP-00372864.
XX
XX 09-DEC-1999; 99JP-00349780.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX WPI; 2001-609968/70.
XX
XX P-PSDB; AAG68116.
XX
XX An IL-1 family protein, used for the development of diagnostic and
XX treatment agents.
XX
XX Claim 2; Page 31-32; 38pp; Japanese.
XX
XX The present sequence encodes a human interleukin 1 (IL-1) family protein
XX having a combining affinity to a receptor of a protein of human IL-1
XX family higher than Tango-77. The protein is useful for the development of
XX diagnostic, treating and/or preventive agents for various diseases
XX
XX Sequence 1104 BP; 328 A; 258 C; 255 G; 263 T; 0 U; 0 Other;
XX
Query Match 79.5%; Score 517; DB 4; Length 1104;
Best Local Similarity 97.2%; Pred. No. 4.6e-159;
Matches 526; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
XX
XX 86 CCGCGAATTCAGCTCTTTGCAAGGTCGAAAGTGAAGAACTTAAACCGAAGAAATTCA 145
XX |||||
XX 491 CCGCCATGAAATTTTGTTCACACAAAGTCAAGGTGAAGAACTTAAACCGAAGAAATTCA 550
XX |||||
XX 146 GGAATTCATGACCAAGATCAAAAGTACGCTGACCTGGGATTCATAGCAGTTTC 205
XX |||||
XX 551 GGAATTCATGACCAAGATCAAAAGTACGCTGACCTGGGATTCATAGCAGTTTC 610
XX |||||
XX 206 CAGATTAATACTACATACGCCCGCAGAGATCTTCTTCATATAGCCTCAGCTCAG 265
XX |||||
XX 611 CAGATTAATACTACATACGCCCGCAGAGATCTTCTTCATATAGCCTCAGCTCAG 670
XX |||||
XX 266 CCTCTGCGGAGAAAGAGTCCGATTCCTCTGCGGAGTCTCTAAAGGAGATTGTCTCT 325
XX |||||
XX 671 CCTCTGCGGAGAAAGAGTCCGATTCCTCTGCGGAGTCTCTAAAGGAGATTGTCTCT 730
XX |||||
XX 326 ACTGTACAAAGGATAAAGGCAAAAGTACATCCCTTCAGCTGGAAGAGAACTCA 385
XX |||||
XX 731 ACTGTACAAAGGATAAAGGCAAAAGTACATCCCTTCAGCTGGAAGAGAACTCA 790
XX |||||
XX 386 TGAAGCTGCGTCCCAAAAGAGATTCAGACGCGGCCCTTCATCTTTTAAGGCTCAGG 445
XX |||||
XX 791 TGAAGCTGCGTCCCAAAAGAGATTCAGACGCGGCCCTTCATCTTTTAAGGCTCAGG 850
XX |||||
XX 446 TGGGCTCTTGGAACATGCTGAGTCCGCGGCTCAACCCCGAGATGTTTCATCTGACCTCCT 505
XX |||||
XX 851 TGGGCTCTTGGAACATGCTGAGTCCGCGGCTCAACCCCGAGATGTTTCATCTGACCTCCT 910
XX |||||

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XX 506 GCAATTTGAATGAGCTGTGGGGTGAACAGATTAATTTGAGAACAGAAACATTTGAT 565
XX |||||
XX 911 GCAATTTGAATGAGCTGTGGGGTGAACAGATTAATTTGAGAACAGAAACATTTGAT 970
XX |||||
XX 566 TTTTCATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTACGCTCAGGATTTGGGTA 625
XX |||||
XX 971 TTTTCATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTACGCTCAGGATTTGAGAA 1030
XX |||||
XX 626 C 626
XX
XX 1031 C 1031
XX
RESULT 5
ADN05011
ID ADN05011 standard; cDNA; 793 BP.
XX
XX ADN05011;
XX
XX 01-JUL-2004 (first entry)
XX
XX Antipsoriatic cDNA sequence #720.
XX
XX ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2004028479-A2.
XX
XX 08-APR-2004.
XX
XX 25-SEP-2003; 2003WO-US030907.
XX
XX 25-SEP-2002; 2002US-0414006P.
XX
XX (GENTH ) GENENTECH INC.
XX
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX Wu TD;
XX
XX WPI; 2004-305105/28.
XX
XX P-PSDB; ADN05012.
XX
XX New PRO-nucleic acid or polypeptide, useful for preparing a
XX pharmaceutical composition for diagnosing or treating psoriasis in a
XX mammal.
XX
XX Claim 1; SEQ ID NO 1405; 3069pp; English.
XX
XX The invention relates to novel polynucleotide and polypeptides for
XX treating psoriasis or a sequence having at least 80% identity to the
XX above sequences. The nucleic acid is useful for preparing a composition
XX for diagnosing or treating psoriasis in a mammal. This sequence
XX corresponds to one of the polynucleotides of the invention.
XX
XX Sequence 793 BP; 241 A; 188 C; 182 G; 182 T; 0 U; 0 Other;
XX
Query Match 79.5%; Score 516.8; DB 12; Length 793;
Best Local Similarity 98.7%; Pred. No. 4.5e-159;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 99 TCTTTGACAGAGTCCCAAGAGTGAAGAACTTAAACCGAAGAAATTCAGATTCAATGACCA 158
XX |||||
XX 183 TGTTCACACAAAGTCCCAAGAGTGAAGAACTTAAACCGAAGAAATTCAGATTCAATGACCA 242
XX |||||
XX 159 GGAATCAAAAGTACTGCTCTGGAATCTGGGAAATCTCATAGCAGTTCCAGATTAATACTA 218
XX |||||
XX 243 GGAATCAAAAGTACTGCTCTGGAATCTGGGAAATCTCATAGCAGTTCCAGATTAATACTA 302
XX |||||
XX 219 CATAGCCCAAGAGATCTTTTTCATTAAGCTTCATCTTGAAGCTCAGCTCTGCGGAGAA 278
XX |||||
XX 303 CATAGCCCAAGAGATCTTTTTCATTAAGCTTCATCTTGAAGCTCAGCTCTGCGGAGAA 362
XX |||||

```

QY 279 AGGAAGTCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTACTGTGACAAGA 338
 DB 363 AGGAAGTCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTACTGTGACAAGA 422
 QY 339 TAAAGACAAGATCATTCATCCCTGAGTGAAGAAAGAACTGATGAAGCTGCTGC 398
 DB 423 TAAAGACAAGATCATTCATCCCTGAGTGAAGAAAGAACTGATGAAGCTGCTGC 482
 QY 399 CCAAAAGATGACGACGCGGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGAA 458
 DB 483 CCAAAAGATGACGACGCGGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGAA 542
 QY 459 CATGCTGAGTGGCGGCTCACCCCGAGATGTTTCACTGCACTCTGCAATTTGATGA 518
 DB 543 CATGCTGAGTGGCGGCTCACCCCGAGATGTTTCACTGCACTCTGCAATTTGATGA 602
 QY 519 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAATTTGAC 578
 DB 603 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAATTTGAC 662
 QY 579 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCTTAAAGGTTAC 626
 DB 663 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCTTAAAGGTTAC 710
 RESULT 6
 AAC66727
 ID AAC66727 standard; cDNA; 802 BP.
 AC AAC66727;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE Human interleukin-1 homologue IL-1H4 coding sequence.
 XX
 KW Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;
 KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
 KW transplant rejection; graft versus host disease; infection; stroke;
 KW ischaemia; acute respiratory disease; allergy; asthma; restenosis;
 KW brain injury; AIDS; bone disease; osteoporosis; cancer;
 KW congestive heart failure; atherosclerosis; Alzheimer's disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200063226-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 14-APR-2000; 2000WO-US010207.
 XX
 PR 16-APR-1999; 99US-00293625.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Young PR, McDonnell PC;
 XX
 DR WPI. 2000-687155/67.
 XX
 P-PSDB; AAB28266.
 XX
 PT Interleukin-1 homolog useful for treating conditions such as chronic and
 PT acute inflammation, septicemia, autoimmune diseases ischemia, acute
 PT respiratory disease, allergies, and asthma.
 XX
 PS Claim 2; Page 28; 30pp; English.
 XX
 CC The present sequence is the coding sequence for human interleukin-1
 CC homologue (IL-1H4). IL-1H4 is useful for treating conditions such as
 CC chronic and acute inflammation, septicemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis, and arthritis), transplant
 CC rejection, graft versus host disease, infection, stroke, ischaemia, acute
 CC respiratory disease, allergies, asthma, restenosis, brain injury, AIDS,
 CC bone diseases (e.g. osteoporosis), cancer, congestive heart failure,

CC atherosclerosis, and Alzheimer's disease, related to either an excess of,
 CC or an under-expression of, IL-1H4 polypeptide activity
 XX
 SQ Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 U; 0 Other;
 Query Match 79.5%; Score 516.8; DB 3; Length 802;
 Best Local Similarity 98.7%; Pred. No. 4,5e-159;
 Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 99 TCTTTGACAGAGTCCAAAGGTGAAGACTTAACCCGAAAGAAATTCAGCATTCATGACCA 158
 DB 192 TCTTTGACAGAGTCCAAAGGTGAAGACTTAACCCGAAAGAAATTCAGCATTCATGACCA 251
 QY 159 GGATCACAAGATGATGCTGCTGGAATCTGGAATCTCATAGAGTTCAGATTAACCTA 218
 DB 252 GGATCACAAGATGATGCTGCTGGAATCTGGAATCTCATAGAGTTCAGATTAACCTA 311
 QY 219 CATAGCCCAAGATCTTCTTTGATTAAGCTCATCTTGAAGCTGAGCTGCGAGAA 278
 DB 312 CATAGCCCAAGATCTTCTTTGATTAAGCTCATCTTGAAGCTGAGCTGCGAGAA 371
 QY 279 AGGAAGTCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTACTGTGACAAGA 338
 DB 372 AGGAAGTCGATTCCTGCGGGCTCTTAAAGGGAGTTTGTCTACTGTGACAAGA 431
 QY 339 TAAAGACAAGATCATTCATCCCTGAGTGAAGAAAGAACTGATGAAGCTGCTGC 398
 DB 432 TAAAGACAAGATCATTCATCCCTGAGTGAAGAAAGAACTGATGAAGCTGCTGC 491
 QY 399 CCAAAAGATGACGACGCGGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGAA 458
 DB 492 CCAAAAGATGACGACGCGGCTTCAATCTTTTATAGGGCTCAGTGGCTCCCTGAA 551
 QY 459 CATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGCACTCTGCAATTTGATGA 518
 DB 552 CATGCTGAGTGGCGGCTCACCCCGAGTGTTCATCTGCACTCTGCAATTTGATGA 611
 QY 519 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAATTTGAC 578
 DB 612 GCCTGTTGGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAATTTGAC 671
 QY 579 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCTTAAAGGTTAC 626
 DB 672 AGTTTGCAAGCTGAATGAGCCCGAGTGAAGTCAAGCTTAAAGGTTAC 719
 RESULT 7
 AAF84120
 ID AAF84120 standard; cDNA; 802 BP.
 AC AAF84120;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Interleukin-1 homologue (IL-1H4) polypeptide encoding cDNA.
 XX
 KW Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
 KW immunosuppressive; antipsoriatic; antiarthritic; cytostatic; antiHIV;
 KW cerebroprotective; antidiabetic; vasotrophic; vulnerable; osteopathic;
 KW immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
 KW gene therapy; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS Location/Qualifiers
 FT 58..714
 FT /*tag= a
 FT /*product= "IL-1H4"
 FT sig_peptide 58..117
 FT /*tag= b
 FT mat_peptide 118..711
 FT /*tag= c

EN WO200140247-A1.
 XX 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US032521.
 XX
 PR 01-DEC-1999; 99US-00452140.
 XX
 XX (SMIR) SMITHKLINE BEECHAM CORP.
 PA
 PI Kumar S, Mcdonnell PC, Young PR;
 XX
 PI WPI, 2001-389949/41.
 DR P-PSDB; AAB85136.
 XX
 XX Novel Interleukin-1 homology, IL-1H4, for treating chronic and acute
 PT inflammation, septicemia, autoimmune diseases, transplant rejection,
 PT graft versus host disease, stroke, ischemia, allergy and asthma.
 XX
 PS Example; Page 29; 30pp; English.

The invention provides an isolated interleukin-1 homologue, IL-1H4
 polypeptide. The IL-1H4 polypeptide can be expressed by standard
 recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
 modulators are useful for treating chronic and acute inflammation,
 septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
 psoriasis and arthritis), transplant rejection, graft versus host
 disease, infection, stroke, ischemia, acute respiratory disease syndrome,
 allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
 osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
 heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
 polynucleotides are useful as diagnostic reagents and for chromosome
 identification. The present sequence represents the cDNA encoding the IL-
 1H4 polypeptide of the invention

Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 U; 0 Other;

Query Match 79.5%; Score 516.8; DB 4; Length 802;
 Best Local Similarity 98.7%; Pred. No. 4.5e-159;
 Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 99 TCTTTGCAAGAGTCCAAAGAGTAAGAACTTAACCGAAGAAATTCAGATTCATGACCA 158
 DB 192 TCTTCAACAAGTCCAAAGAGTAAGAACTTAACCGAAGAAATTCAGATTCATGACCA 251
 QY 159 GGATCAACAAGTACTGCTCTGAGCTCTGGGAATCATAGCAAGTTCAGATTAATAACTA 218
 DB 253 GGATCAACAAGTACTGCTCTGAGCTCTGGGAATCATAGCAAGTTCAGATTAATAACTA 311
 QY 219 CATAGCCCAAGATCTTCTTGATTAAGCTTCATCTTACCTAGCTCTGCGAGAA 278
 DB 312 CATAGCCCAAGATCTTCTTGATTAAGCTTCATCTTACCTAGCTCTGCGAGAA 371
 QY 279 AGGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTCTCTCTGAGCAAGA 338
 DB 372 AGGAAGTCCGATTCCTGCGGGGCTCTTAAGGGAGTTTCTCTCTGAGCAAGA 431
 QY 339 TAAAGCAACAAGTCAATCCCTTCAAGCTGAGAAAGAAATCATAGTAAAGCTGCTGC 398
 DB 432 TAAAGCAACAAGTCAATCCCTTCAAGCTGAGAAAGAAATCATAGTAAAGCTGCTGC 491
 QY 399 CCAAAAAGATGACGCGCGGCTCTTATAGGGCTCAAGTGGGCTCTCTGANA 458
 DB 492 CCAAAAAGATGACGCGCGGCTCTTATAGGGCTCAAGTGGGCTCTCTGANA 551
 QY 459 CATGCTGAGTGGGCGGCTCAACCGGAGTTCATCTGACACTCTGAAATTTGTAATGA 518
 DB 552 CATGCTGAGTGGGCGGCTCAACCGGAGTTCATCTGACACTCTGAAATTTGTAATGA 611
 QY 519 GCGCTGTTGGGGTGACAGATTAATTTGAGAAAGAAACATTTGATTTTCAATTCACAC 578
 DB 612 GCGCTGTTGGGGTGACAGATTAATTTGAGAAAGAAACATTTGATTTTCAATTCACAC 671

QY 579 AGTTTGCAAGAGTGAATGAGCCCGAGTGAGTCAAGCATTAAGGCTAC 626
 DB 672 AGTTTGCAAGAGTGAATGAGCCCGAGTGAGTCAAGCATTAAGGAAAC 719

RESULT 8

AAA51604 standard; DNA, 839 BP.

AAA51604;

31-OCT-2000 (first entry)

Human IL-1 receptor antagonist 1 V DNA.

hIL-1Ra1v; human interleukin-1 receptor antagonist-1; IL-1Ib;
 anti-osteoporosis; interleukin-1-like polypeptide; anti-inflammatory;
 anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
 anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 gene therapy; ds.

Homo sapiens.

Location/Qualifiers

73..729

/*tag= a

/product= "hIL-1Ra1v"

/partial

MO200039297-A2.

06-JUL-2000.

22-DEC-1999; 99WO-US030720.

23-DEC-1998; 98US-0113430P.

22-JAN-1999; 99US-0116843P.

13-APR-1999; 99US-0129122P.

(GETH) GENENTECH INC.

Goddard A, Pan J;

WPI, 2000-452395/39.

P-PSDB; AAY96940.

Nucleic acids encoding interleukin-1-like polypeptides, useful for

preventing and treating e.g. inflammation, asthma and psoriasis.

Claim 7, Fig 19; 143pp; English.

An isolated nucleic acid molecule encoding an interleukin-1-like

polypeptide (IL-1Ib) that retains one or more activities of the peptide

from which it is derived, such as the IL-1Ib binding activity of a human

interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The

nucleic acids may be used in molecular engineering applications, e.g.

hybridization assays and chromosome and gene mapping studies, for

recombinantly producing the IL-1Ib polypeptide or for producing gene

knock out animals to study the role of the protein in metabolism and

disease processes (conversely, gene therapy protocols may be used to

supplement a patient's production of the polypeptide or to rectify

mutations that lead to the production of in active peptides). The

peptides produced may be used to screen for and produce modulators (e.g.

antibodies) of IL-1Ib protein expression and activity which may be used to

treat disorders associated with inappropriate IL-1Ib expression and

activity, such as inflammatory disorders, asthma, arthritis,

osteoarthritis, sepsis, acute lung injury, adult respiratory distress

syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,

psoriasis, graft versus host disease and/or inflammatory bowel disease

Sequence 839 BP; 249 A; 202 C; 196 G; 192 T; 0 U; 0 Other;

Query Match 79.5%; Score 516.8; DB 3; Length 839;

Best Local Similarity 98.7%; Pred. No. 4.6e-159;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
OY 99 TCTTTGACAGAGTCCCAAGGTGAAGACTTAACCCGAGAAATTCAGATTCATACCA 158
DB 207 TGTTCACACAAAGTCCAAAGGTGAAGACTTAACCCGAGAAATTCAGATTCATACCA 266
OY 159 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGAGTCCAGATTAACCTA 218
DB 267 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGAGTCCAGATTAACCTA 326
OY 219 CATAGCCCAAGAGATCTTCTTGATTAAGCTTCATCTTGAAGCTCTGCGGAGAA 278
DB 327 CATAGCCCAAGAGATCTTCTTGATTAAGCTTCATCTTGAAGCTCTGCGGAGAA 386
OY 279 AGGAGTCCGATTCCTCTGAGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 338
DB 387 AGGAGTCCGATTCCTCTGAGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 446
OY 339 TAAAGGACAAAGTCAATCCCTTCAAGCTGAAGAGAACTGATGAAGCTGCTGC 398
DB 447 TAAAGGACAAAGTCAATCCCTTCAAGCTGAAGAGAACTGATGAAGCTGCTGC 506
OY 399 CCAAAAGGATGACAGCGCCGCTTCACTTTTATAGGCTCAAGTGGCTCTCTGAA 458
DB 507 CCAAAAGGATGACAGCGCCGCTTCACTTTTATAGGCTCAAGTGGCTCTCTGAA 566
OY 459 CATGCTGAGTGGGCGCTCAACCCGAGATGTTTCATCTGACACTCTGCAATTTGATGA 518
DB 567 CATGCTGAGTGGGCGCTCAACCCGAGATGTTTCATCTGACACTCTGCAATTTGATGA 626
OY 519 GCCTGTGGGGTGACAGATTAATTTGAGAAACAGAAACATTGAATTTTCAATTCACAC 578
DB 627 GCCTGTGGGGTGACAGATTAATTTGAGAAACAGAAACATTGAATTTTCAATTCACAC 686
OY 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGCTGAGGATAGGATAC 626
DB 687 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGCTGAGGATAGGATAGGATAC 734
```

RESULT 9

AAD00210
ID AAD00210 standard; cDNA; 1600 BP.

AC AAD00210;

XX 05-SEP-2000 (first entry)

DE Human zilla4 cDNA.

XX Human interleukin-1, IL-1, zilla4 protein; inflammation; arthritis;
XX psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
XX anaemia; inflammatory bowel disease; acute neuropathology; shock;
XX chronic neuropathology; respiratory disease syndrome; restenosis;
XX acquired immune deficiency syndrome; AIDS; anti-inflammatory; cyclostatic;
XX anti-arthritis; anti-psoriasis; antibacterial; immunosuppressive;
XX anti-anaemic; neuroprotective; vasotropic;
XX anti-human immunodeficiency virus; HIV; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Key 447..1503

XX Key /tag= a

XX Key /product= "Human zilla4 protein"

XX PD 04-MAY-2000.

XX PF 27-OCT-1999; 99WO-US025038.

XX PR 27-OCT-1998; 98US-00179614.

XX (ZYMO) ZYMOGENETICS INC.

PI West RR, Sheppard PO, Gao Z;

XX MPI; 2000-350740/30.

XX P-PSDB; AAY70927.

PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukaemia.

XX Example 2; Page 61-63; 88pp; English.

CC The present cDNA sequence encodes human interleukin (IL)-1 homolog zilla4
CC protein. This cDNA was cloned from a human foetal lung cDNA library. The
CC zilla4 proteins modulate inflammation and other immunological processes
CC and are therefore useful for treatment of arthritis, psoriasis, septic
CC shock, graft-versus-host disease and leukaemia. Other diseases that may
CC be modulated by zilla4 proteins include cancer, anaemia, inflammatory
CC bowel disease, acute and chronic neuropathologies, shock, respiratory
CC disease syndrome, restenosis and acquired immune deficiency syndrome

XX Sequence 1600 BP; 481 A; 356 C; 378 G; 385 T; 0 U; 0 Other;

Query Match 79.5%; Score 516.8; DB 3; Length 1600;

Best Local Similarity 98.7%; Pred. No. 6.6e-159;

Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
OY 99 TCTTTGACAGAGTCCCAAGGTGAAGACTTAACCCGAGAAATTCAGATTCATACCA 158
DB 981 TGTTCACACAAAGTCCAAAGGTGAAGACTTAACCCGAGAAATTCAGATTCATACCA 1040
OY 159 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGAGTCCAGATTAACCTA 218
DB 1041 GGATCAACAAAGTACTGCTCTGAGACTCTGGAATCTCATAGAGTCCAGATTAACCTA 1100
OY 219 GCCTGTGGGGTGACAGATTAATTTGAGAAACAGAAACATTGAATTTTCAATTCACAC 578
DB 1101 GCCTGTGGGGTGACAGATTAATTTGAGAAACAGAAACATTGAATTTTCAATTCACAC 686
OY 279 AGGAGTCCGATTCCTCTGAGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 338
DB 1161 AGGAGTCCGATTCCTCTGAGGCTCTTAAGGGAGTTTGTCTTACTGTGACAAAGA 1220
OY 339 TAAAGGACAAAGTCAATCCCTTCAAGCTGAAGAGAACTGATGAAGCTGCTGC 398
DB 1221 TAAAGGACAAAGTCAATCCCTTCAAGCTGAAGAGAACTGATGAAGCTGCTGC 1280
OY 399 CCAAAAGGATGACAGCGCCGCTTCACTTTTATAGGCTCAAGTGGCTCTCTGAA 458
DB 1281 CCAAAAGGATGACAGCGCCGCTTCACTTTTATAGGCTCAAGTGGCTCTCTGAA 1340
OY 459 CATGCTGAGTGGGCGCTCAACCCGAGATGTTTCATCTGACACTCTGCAATTTGATGA 518
DB 1341 CATGCTGAGTGGGCGCTCAACCCGAGATGTTTCATCTGACACTCTGCAATTTGATGA 1400
OY 519 GCCTGTGGGGTGACAGATTAATTTGAGAAACAGAAACATTGAATTTTCAATTCACAC 578
DB 1401 GCCTGTGGGGTGACAGATTAATTTGAGAAACAGAAACATTGAATTTTCAATTCACAC 1460
OY 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGCTGAGGATAGGATAC 626
DB 1461 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGCTGAGGATAGGATAGGATAC 1508
```

RESULT 10

ADH89066
ID ADH89066 standard; DNA; 1600 BP.

XX ADH89066;

XX 22-APR-2004 (first entry)

XX	DE	DNA encoding human z11a4 polypeptide.
XX	KW	Human; interleukin-1 homologue; IL-1; z11a4; immune response;
XX	KW	inflammatory disease; cancer; anaemia; immunomodulator; antiinflammatory;
XX	KW	cytostatic; antianaemic; chromosome 2; gene; ds.
XX	OS	Homo sapiens.
XX	PH	Key
XX	FT	CDS
XX	FT	847..1503
XX	FT	/tag= a
XX	FT	/product= "z11a4"
XX	PN	US2003148467-A1.
XX	XX	
XX	PD	07-AUG-2003.
XX	PF	22-NOV-2002; 2002US-00302554.
XX	PR	27-OCT-1998; 98US-0105824P.
XX	PR	27-OCT-1999; 99US-00428118.
XX	PA	(Zymo) ZYMOGENETICS INC.
XX	PI	West RR, Sheppard PO, Gao Z;
XX	DR	WPI; 2003-897576/82.
XX	DR	P-PSDB; ADH89067.
XX	PT	New interleukin-1 homolog z11a4 protein, useful for modulating an immune
XX	PT	response and for treating diseases, e.g., inflammatory diseases, cancer
XX	PT	or anemia.
XX	PS	Example 2; SEQ ID NO 1; 44p; English.
XX	CC	The present invention relates to the isolation of human interleukin-1 (IL
XX	CC	-1) homologues designated z11a4, and the polynucleotide sequences that
XX	CC	encode them. The gene encoding human z11a4 is located on chromosome 2.
XX	CC	Also disclosed is a method of making these proteins and a method of
XX	CC	modulating an immune response. The proteins are useful for treating
XX	CC	diseases such as inflammatory diseases, cancer, and anaemia. The present
XX	CC	sequence encodes human z11a4.
XX	SQ	Sequence 1600 BP; 481 A; 356 C; 378 G; 385 T; 0 U; 0 Other;
QY		Query Match 79.5%; Score 516.8; DB 10; Length 1600;
		Best Local Similarity 98.7%; Pred. No. 6.6e-159;
		Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	99	TCCTTTCGAGAGGTCCAAAGGTGAAGACTTAACCCGAAAGAAATTCAGCATTCATGACCA 158
DB	981	TGTTTCACACAAAGTCGCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAACCA 1040
QY	159	GGATTCACAAAGTATCTGCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAACCA 218
DB	1041	GGATTCACAAAGTATCTGCTGAGACTCTGGAATCTCATAGCAGTTCAGATTAACCA 1100
QY	219	CATAGCCGACGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCAGCCTCGGGAA 278
DB	1101	CATAGCCGACGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCAGCCTCGGGAA 1160
QY	279	AGGAAGTCGATCTCTCTGGGGGTCTTAAAGGGAGTTTGTCTTACTGTGACAGGA 338
DB	1161	AGGAAGTCGATCTCTCTGGGGGTCTTAAAGGGAGTTTGTCTTACTGTGACAGGA 1220
QY	339	TAAAGGACAAAGTCATCCCTTAGCTGGAAGAGGAAGTGAAGAGTGGCTGC 398
DB	1221	TAAAGGACAAAGTCATCCCTTAGCTGGAAGAGGAAGTGAAGAGTGGCTGC 1280
QY	399	CCAAAAGGATCGACAGCGCGGCTTCACTTTTAAAGGCTCAGTGGCTCCTGGA 458
DB	1281	CCAAAAGGATCGACAGCGCGGCTTCACTTTTAAAGGCTCAGTGGCTCCTGGA 1340

QY	459	CATGTCGAGTCGGGGGCTCAACCCCGAGTGGTTATCTCGAACCTCTCGAATTGTAAATGA	511
Db	1341	CATGTCGAGTCGGGGGCTCAACCCCGAGTGGTTATCTCGAACCTCTCGAATTGTAAATGA	1401
QY	519	GCTGTTCGGGGTGCACAGATAATTGTAGAAACAGAAACACATTTGAATTTTCATTTCACCC	578
Db	1401	GCTGTTCGGGGTGCACAGATAATTGTAGAAACAGAAACACATTTGAATTTTCATTTCACCC	1461
QY	579	AGTTTGCAGAGCTGAAATGAGCCCCAGTGAAGTTCAGCGATTAGGGGTAC	626
Db	1461	AGTTTGCAGAGCTGAAATGAGCCCCAGTGAAGTTCAGCGATTAGGGGTAC	1508
RESULT 11			
AAA27918	ID	AAA27918 standard; cDNA, 579 BP.	
XX	AC	AAA27918;	
XX	DT	12-SEP-2000 (first entry)	
DE	XX	Human interleukin-1 zeta cDNA coding region.	
XX	XX	Interleukin-1 zeta; IL-1 zeta; human; chromosome 2; gene therapy;	
KW	XX	glaucoma; ectodermal dysplasia; winkly skin syndrome;	
KW	XX	insulin-dependent diabetes mellitus; leukaemia; lymphoma;	
KW	XX	tibial muscular dystrophy; ss.	
OS	XX	Homo sapiens.	
PN	XX	WO200036108-A2.	
PD	XX	22-JUN-2000.	
PF	XX	14-DEC-1999; 99WO-US029549.	
PR	XX	14-DEC-1998; 98US-0112163P.	
PR	XX	10-NOV-1999; 99US-0164675P.	
PA	XX	(IMMV) IMMUNEX CORP.	
PI	XX	Sims JE, Smith DE, Born TL;	
DR	XX	WPI; 2000-442387/38.	
DR	XX	P-PSDB; AAY95297.	
PT	XX	Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants	
PT	XX	TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for	
PT	XX	identifying genes associated with diseases such as glaucoma, and insulin-	
PT	XX	dependent diabetes mellitus.	
PS	XX	Claim 1(a); Page 8; 87pb; English.	
CC	XX	The present sequence is that of the coding region of cDNA encoding human	
CC	XX	interleukin-1 zeta (IL-1 zeta, see AAY95297), a member of the IL-1	
CC	XX	family. The sequence was deduced from EST IMAGE clone 1628791, which	
CC	XX	encodes a partial open reading frame, and from additional sequences	
CC	XX	obtained from PCR and 5' RACE reactions. IL-1 zeta mRNA is generated from	
CC	XX	exons 3-6 of the IL-1 zeta locus. The mRNA is expressed most strongly in	
CC	XX	the testis, prostate, colon, brain, placenta, lung, foetal liver and	
CC	XX	lymph node. The invention is directed to novel, purified and isolated IL-	
CC	XX	1 zeta, IL-1 zeta splice variants and Xrec2 polypeptides (see AAY95297-	
CC	XX	301), the nucleic acids (see AAA27918-22) encoding such polypeptides,	
CC	XX	processes for production of recombinant forms of such polypeptides, and	
CC	XX	their uses. IL-1 zeta nucleic acids are used to: to express IL-1 zeta	
CC	XX	polypeptides; as probes to identify nucleic acids encoding proteins of	
CC	XX	the IL-1 ligand family; to identify human chromosome 2; to map genes on	
CC	XX	chromosome 2; to identify genes associated with diseases, syndromes, or	
CC	XX	other conditions associated with chromosome 2, such as glaucoma,	
CC	XX	ectodermal dysplasia, insulin-dependent diabetes mellitus, winkly skin	
CC	XX	syndrome, T-cell leukaemia or lymphoma, and tibial muscular dystrophy; as	
CC	XX	single-stranded sense or antisense oligonucleotides to inhibit expression	


```
XX WO200017363-A2.
PN
XX
XX 30-MAR-2000.
PD
XX 17-SEP-1999; 99WO-US020868.
XX
XX 18-SEP-1998; 98US-00156966.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Timans JC;
XX
XX MPI; 2000-283588/24.
XX
XX P-PSDB; AAY91885.
XX
XX New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
PT sequence.
XX
XX
XX PS Disclosure; Page 102-103; 110pp; English.
XX
XX The present sequence encodes a primate interleukin-1 like molecule,
CC designated IL-1-zeta. It is an alternative sequence to AAA08512, perhaps
CC an allelic variant. The specification claims an isolated or recombinant
CC polypeptide that: (a) specifically binds polyclonal antibodies generated
CC against at least a 12 consecutive amino acid segment of IL-1-zeta (see
CC AAY91884) or its allelic variant (see AAY91885); and (b) comprises at
CC least one sequence selected from: AAY91886-903 or AAY91904-06. The
CC preferred 12 consecutive amino acid segment is chosen from AAY91907-18 or
CC AAY91919-21. IL-1-zeta is likely to play a role in systemic inflammatory
CC reactions, such as fever, hypoglycemia, reduced plasma iron and zinc, the
CC acute response of the liver, and increase plasma copper. IL-1-zeta
CC binding compounds (comprising antigen binding sites) and IL-1-zeta
CC polypeptides are also useful for both diagnostic and therapeutic purposes
XX
XX Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 U; 0 Other;
SQ
Query Match 79.3%; Score 515.2; DB 3; Length 657;
Best Local Similarity 97.6%; Pred. No. 1.4e-158;
Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 86 CCGCGAATTCAGCTCTTGGCAGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 145
DB 122 CCGCATGAATTTGTTTTCACACAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 181
QY 146 GCATTCATACCAAGATCAACAAAGTACTGCTCTGACCTCTGGAAATTCATAGCAGTTTC 205
DB 182 GATTCATACCAAGATCAACAAAGTACTGCTCTGACCTCTGGAAATTCATAGCAGTTTC 241
QY 206 CAGATTAATACTACATACGCGCCAGAGATCTCTTTCATTAAGCTTCATAGGCTCAG 265
DB 242 CAGATTAATACTACATACGCGCCAGAGATCTCTTTCATTAAGCTTCATAGGCTCAG 301
QY 266 CCTCTCCGAGAAAGAGTCCGATTCCTCTGGGGGCTCTCTAAAGGGAGTTTGTCTCT 325
DB 302 CCTCTCCGAGAAAGAGTCCGATTCCTCTGGGGGCTCTCTAAAGGGAGTTTGTCTCT 361
QY 326 ACTGTGACAAAGATTAAGACAAAGTATCATCTCTTCACTGAGTGAAGAGAGAACTGA 385
DB 362 ACTGTGACAAAGATTAAGACAAAGTATCATCTCTTCACTGAGTGAAGAGAGAACTGA 421
QY 386 TGAAGTGTGCTGCGCCAAAGAGATCAGCGCGGCTTCATCTTTTAAGGGCTCAGG 445
DB 422 TGAAGTGTGCTGCGCCAAAGAGATCAGCGCGGCTTCATCTTTTAAGGGCTCAGG 481
QY 446 TGGGCTCTTGAACATAGCTGAGTCCGCGGCTCACCCCGAGATGTTTCATTCGACCTCT 505
DB 482 TGGGCTCTTGAACATAGCTGAGTCCGCGGCTCACCCCGAGATGTTTCATTCGACCTCT 541
QY 506 GCAATTTGTAATGAGCTGTTGGGGTGAAGATTAATTTGAGAAACAGAGAAACACATTGAAT 565
DB 542 GCAATTTGTAATGAGCTGTTGGGGTGAAGATTAATTTGAGAAACAGAGAAACACATTGAAT 601
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QY 566 TTTTCATTTCAACCAAGTTTGCAAGCTGAATGAGCCCGAGTGAAGCGATTTAG 621
DB 602 TTTTCATTTCAACCAAGTTTGCAAGCTGAATGAGCCCGAGTGAAGCGATTTAG 657
RESULT 14
ADJ88305
ID ADJ88305 strand; DNA; 657 BP.
XX
XX ADJ88305;
AC
XX 06-MAY-2004 (first entry)
XX
XX Human interleukin-1zeta DNA variant.
XX
XX Interleukin-1zeta, gene therapy; immune system; haematopoietic cell;
KW inflammatory disorder; infection; allergy; cancer; human; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 1..657
FT /tag= a
FT /product= "Human IL-1zeta variant"
XX
XX US6680380-B1.
PD 20-JAN-2004.
XX
XX 17-SEP-1999; 99US-00398412.
XX
XX 18-SEP-1998; 98US-0100948P.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Timans JC;
XX
XX MPI; 2004-189656/18.
XX
XX P-PSDB; ADJ88306.
XX
XX New nucleic acid molecules encoding mammalian interleukin-1 polypeptides,
PT useful for diagnosing, preventing or treating diseases associated with
PT abnormal expression of interleukin, e.g. inflammation, infection or
PT cancer.
XX
XX Claim 1, SEQ ID NO 3; 36pp; English.
XX
XX The invention relates to an isolated or recombinant nucleic acid encoding
CC interleukin-1zeta polypeptide. The invention is useful in gene therapy.
CC The composition and methods are useful in diagnosing or treating
CC degenerative or abnormal conditions which directly or indirectly involve
CC development, differentiation or function, e.g. of the immune system
CC and/or haematopoietic cells. The invention may also be used for
CC preventing or treating other diseases or disorders associated with
CC abnormal expression or triggering of response to the interleukin, such as
CC inflammatory disorders, infection, allergies or cancer. The present
CC sequence is human interleukin-1zeta DNA variant.
XX
XX Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 U; 0 Other;
SQ
Query Match 79.3%; Score 515.2; DB 12; Length 657;
Best Local Similarity 97.6%; Pred. No. 1.4e-158;
Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 86 CCGCGAATTCAGCTCTTGGCAGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 145
DB 122 CCGCATGAATTTGTTTTCACACAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCA 181
QY 146 GCATTCATACCAAGATCAACAAAGTACTGCTCTGACCTCTGGAAATTCATAGCAGTTTC 205
DB 182 GATTCATACCAAGATCAACAAAGTACTGCTCTGACCTCTGGAAATTCATAGCAGTTTC 241
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QY 206 CAGATATAAACTACATACGCCAGAGATCTTTTCATTAAGCCATCTCTTGAAGCTCAG 265
 DB 242 CAGATATAAACTACATACGCCAGAGATCTTTTCATTAAGCCATCTCTTGAAGCTCAG 301
 QY 266 CCTCTCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGAGTTTGTCTCT 325
 DB 302 CCTCTCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGAGTTTGTCTCT 361
 QY 326 ACTGTACAAAGATTAAGGACAAAGTCATCCCTTCAGCTGAGAAAGAGAAACTGA 385
 DB 362 ACTGTACAAAGATTAAGGACAAAGTCATCCCTTCAGCTGAGAAAGAGAAACTGA 421
 QY 386 TGAAGCTGCTGCGCCAAAAGAAATGACACGCCGCGCTTCATCTTTATAGGGCTCAG 445
 DB 422 TGAAGCTGCTGCGCCAAAAGAAATGACACGCCGCGCTTCATCTTTATAGGGCTCAG 481
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 DB 482 TGGGCTCTCGAAACATGCTGAGAGTGGCGGCTCAACCCGGATGCTTCATCTGCACTCT 541
 QY 506 GCAATTTGTAATGAGCTGTTGGGGTGACAGATTAATTTTGAGAACAGGAAACATTTGAAT 565
 DB 542 GCAATTTGTAATGAGCTGTTGGGGTGACAGATTAATTTTGAGAACAGGAAACATTTGAAT 601
 QY 566 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 621
 DB 602 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 657

RESULT 15

ADL15867
 ID ADL15867 standard; cDNA; 657 BP.

AC ADL15867;

DT 01-JUL-2004 (first entry)

DE Human interleukin 1 zeta (IL-1zeta) cDNA seqid 3.

XX antiinflammatory; interleukin 1 zeta; IL-1 zeta; immunogen;

KM antisera production; antibody production; anti-inflammatory; human; gene;

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..657

FT /tag= a

FT /product= "IL-1 zeta"

FT /note= "Interleukin 1 zeta"

XX US2004068099-A1.

XX 08-APR-2004.

XX 27-OCT-2003; 2003US-00695195.

XX 18-SEP-1998; 98US-0100948P.

XX 17-SEP-1999; 99US-00398412.

XX (TIMA/) TIMANS J C.

XX Timans JC;

XX WPI; 2004-304623/28.

XX P-PSDB; ADL15868.

XX Novel isolated or recombinant interleukin 1 zeta polypeptide useful as
 PT immunogen for producing specific antibodies or for developing anti-
 PT inflammatory therapeutics.
 PS Claim 14; SEQ ID NO 3; 42pp; English.
 XX

CC The invention describes an isolated or recombinant interleukin 1 zeta
 CC polypeptide (I) that specifically binds to polyclonal antibodies
 CC generated against at least a 12 consecutive amino acid segment of two
 CC fully defined sequences (S1) and (S2) having 218 amino acids as given in
 CC the specification and comprises at least one sequence chosen from (S1)
 CC and (S2). Also described are: a fusion protein comprising (I) or its
 CC sequences, a detection or purification tag, including FLAG, His6 or Ig
 CC sequence or sequence of another cytokine or chemokine; a binding compound
 CC (II) an antigen binding site from an antibody, which specifically binds
 CC to (I); a composition of matter comprising a sterile polypeptide (I) or
 CC (II), (I) or (II) and a carrier such as an aqueous compound e.g., water,
 CC saline and/or buffer, where the carrier is formulated for oral, rectal,
 CC nasal, topical or parental administration; an isolated or recombinant
 CC nucleic acid (III) that encodes (I) or several antigenic peptides of (S1)
 CC or (S2); a cell (IV) transformed with (III); a method of modulating a
 CC cell involved in an inflammatory response, by contacting the cell with an
 CC agonist or antagonist of (I); a kit comprising a compartment of (I), (II)
 CC or (III) and/or instructions for use or disposal of reagents in the kit;
 CC and producing an antibody as mentioned in (II) or an antigen-antibody
 CC complex. (I) is useful as immunogen for producing antisera or specific
 CC antibodies or useful for developing more effective anti-inflammatory
 CC therapeutics. This sequence encodes a human interleukin 1 zeta
 CC polypeptide.
 CC
 XX

Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 U; 0 Other;

Query Match 79.3%; Score 515.2; DB 12; Length 657;

Best Local Similarity 97.6%; Pred. No. 14e-158; Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 86 CCGCAATTCAGCTCTTTGACAGAGTCCAAAGTGAAGAACTTAAACCGAAGAAATTGA 145
 DB 122 CCGCATGAATTTTGTTCACACAGATCCAAAGTGAAGAACTTAAACCGAAGAAATTGA 181
 QY 146 GCAATTCATGACCAAGATCAAAAGTACTGCTGAGCTTGGAAATCTCATGACAGTTT 205
 DB 182 GCAATTCATGACCAAGATCAAAAGTACTGCTGAGCTTGGAAATCTCATGACAGTTT 241
 QY 206 CAGATATAAACTACATACGCCAGAGATCTTTTCATTAAGCCATCTCTTGAAGCTCAG 265
 DB 242 CAGATATAAACTACATACGCCAGAGATCTTTTCATTAAGCCATCTCTTGAAGCTCAG 301
 QY 266 CCTCTCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 325
 DB 302 CCTCTCGGAGAAAGAAAGTCCGATTTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCT 361
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 QY 566 TTTCAATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCAAGTGAAGTCAAGCAATTAG 621
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SUMMARIES

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1	516.8	79.5	802	3	US-09-293-625-1 Sequence 1, Appl1
2	515.2	79.3	657	4	US-09-398-412B-3 Sequence 3, Appl1
3	510.4	78.5	1225	4	US-09-398-412B-1 Sequence 1, Appl1
4	397	61.1	989	3	US-09-128-155-1 Sequence 1, Appl1
5	392.2	60.3	408	3	US-09-128-155-10 Sequence 10, Appl1
6	392.2	60.3	501	3	US-09-128-155-6 Sequence 6, Appl1
7	392.2	60.3	534	3	US-09-128-155-3 Sequence 3, Appl1
8	252.8	38.9	176373	3	US-09-128-155-17 Sequence 17, Appl1
9	69	10.6	204	1	US-08-330-638D-1 Sequence 1, Appl1
10	69	10.6	204	2	US-08-906-746A-1 Sequence 1, Appl1
11	69	10.6	1479	1	US-08-644-271-31 Sequence 31, Appl1
12	69	10.6	1479	3	US-09-077-955-35 Sequence 35, Appl1
13	63.2	9.7	96	1	US-07-977-451-7 Sequence 7, Appl1
14	63.2	9.7	96	1	US-08-252-517-7 Sequence 7, Appl1
15	63.2	9.7	96	1	US-08-601-891-7 Sequence 7, Appl1
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18	63.2	9.7	96	4	US-09-872-136B-8 Sequence 8, Appl1
19	63.2	9.7	96	5	PCT-US92-09893-7 Sequence 8, Appl1
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25	54.2	8.3	59	3	US-09-260-038B-9 Sequence 9, Appl1
26	54.2	8.3	59	3	US-09-635-923-9 Sequence 9, Appl1
27	54.2	8.3	59	4	US-09-487-716A-9 Sequence 9, Appl1

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32	51.2	7.9	1183	3	US-09-069-619-1 Sequence 1, Appl1
33	51.2	7.9	1183	3	US-09-494-018-1 Sequence 1, Appl1
34	49.4	7.6	53	3	US-09-260-038B-10 Sequence 10, Appl1
35	49.4	7.6	53	3	US-09-635-923-10 Sequence 10, Appl1
36	49.4	7.6	53	4	US-09-487-716A-10 Sequence 10, Appl1
37	48.6	7.5	585	4	US-09-976-472A-1 Sequence 1, Appl1
38	48.4	7.4	50	3	US-09-260-038B-12 Sequence 12, Appl1
39	48.4	7.4	50	3	US-09-635-923-12 Sequence 12, Appl1
40	48.4	7.4	50	4	US-09-487-716A-12 Sequence 12, Appl1
41	47.6	7.3	477	4	US-09-970-033-7 Sequence 7, Appl1
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43	45	6.9	45	4	US-10-105-080-16 Sequence 16, Appl1
44	45	6.9	802	4	US-09-949-016-2899 Sequence 2899, Appl1
45	43.4	6.7	301	3	US-09-386-642-2 Sequence 2, Appl1

ALIGNMENTS

RESULT 1									
US-09-293-625-1									
; Sequence 1, Application US/09293625									
; Patent No. 6342371									
; GENERAL INFORMATION:									
; APPLICANT: Young, Peter R.									
; APPLICANT: McDonnell, Peter C									
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4									
; FILE REFERENCE: GP-70607									
; CURRENT APPLICATION NUMBER: US/09/293,625									
; NUMBER OF SEQ ID NOS: 2									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO 1									
; LENGTH: 802									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
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Query Match 79.5%; Score 516.8; DB 3; Length 802;									
Best Local Similarity 98.7%; Pred. No. 6.4e-152;									
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
QY	99	TCCTTGACAGAGTCCAAAGTGAAGACTTAAACCGAAGAAATTCAGATTATGACCA	158						
DB	192	TTCTTACACAAAGTCCAAAGTGAAGACTTAAACCGAAGAAATTCAGATTATGACCA	251						
QY	159	GGATCACAAAGTACTGCTCTGAGATCTTGGAAATTCATAGAGTTCCAGATTAATACTA	218						
DB	252	GGATCACAAAGTACTGCTCTGAGATCTTGGAAATTCATAGAGTTCCAGATTAATACTA	311						
QY	219	CATACGCCAGAGATCTTGTGATTAAGCCATCTTGAAGCTCAGCCTCGCGAGAA	278						
DB	312	CATACGCCAGAGATCTTGTGATTAAGCCATCTTGAAGCTCAGCCTCGCGAGAA	371						
QY	279	AGGAAGTCGATTCCTGCGGGGCTCTTAAAGGGAGTTTGTCTTCTATGACAAGGA	338						
DB	372	AGGAAGTCGATTCCTGCGGGGCTCTTAAAGGGAGTTTGTCTTCTATGACAAGGA	431						
QY	339	TAAAGACAAAGTCAATCCATCTTCAAGCTGAAGAAAGAACTGATGAAGCTGCTGC	398						
DB	432	TAAAGACAAAGTCAATCCATCTTCAAGCTGAAGAAAGAACTGATGAAGCTGCTGC	491						
QY	399	CCAAAGGATGAGACGCGGCTCTTATATAGGGCTGAGGGCTCTTGGA	458						
DB	492	CCAAAGGATGAGACGCGGCTCTTATATAGGGCTGAGGGCTCTTGGA	551						
QY	459	CATGCTGAGTCCGCGGCTCAACCCGAGATGTTCACTGCACTTCTGCAATTTGATGA	518						
DB	552	CATGCTGAGTCCGCGGCTCAACCCGAGATGTTCACTGCACTTCTGCAATTTGATGA	611						

QY	Db	QY	Db
519	612	579	672
GCGTGTGGGGGACAGATTAATTTGAGAAACGGAAACACATTTAAATTTATTTCAAC	GCGTGTGGGGGACAGATTAATTTGAGAAACGGAAACACATTTAAATTTATTTCAAC	AGTTTTCGCAAAAGCTGAATATGAGCCCAAGTAGAGTCAAGCATTTAGGGTAC	AGTTTTCGCAAAAGCTGAATATGAGCCCAAGTAGAGTCAAGCATTTAGGAAC
578	671	626	719

RESULT 2
US-09-39

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? Sequence 3, Application US/09398412B
? Patent No. 6680380
? GENERAL INFORMATION:
? APPLICANT: Timans, Jacqueline C.
? TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
? TITLE OF INVENTION: methods
? FILE REFERENCE: DX0904K
? CURRENT APPLICATION NUMBER: US/09/398,412B
? CURRENT FILING DATE: 1999-09-17
? PRIOR APPLICATION NUMBER: US 60/100948
? PRIOR FILING DATE: 1998-09-18
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: patentIn version 3.1
? SEQ ID NO 3
? LENGTH: 657
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(654)
? OTHER INFORMATION:
? US-09-398-412B-3

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Query Match	79.3%	Score 515.2	DB 4	Length 657
Best Local Similarity	97.6%	Pred. 1.9e-151		
Matches 523	Conservative	0	Mismatches 13	Indels 0
				Gaps 0

Oy	8	CGCGAAATTCAGCTCTTTGACAGGGTCCAAAGTAAACACTTAAACCCGAAATTTCA	145
Db	122	CGCGCATGAATTTTGTTCACACAGTCCAAAGGTAAAGACTTAAACCCGAAATTTCA	181
Oy	146	GCATTCATGACCCAGATCACAAAGTACTGTTCTTGAACTCTGGAAATCTCATAGACTTC	205
Db	182	GCATTCATGACCCAGATCACAAAGTACTGTTCTTGAACTCTGGAAATCTCATAGACTTC	241
Oy	206	CAGATTAATACTACATAGCCCAAGAGATTTCTTTGCATTAGCTCATCTTGAGCTCAG	265
Db	242	CAGATTAATACTACATAGCCCAAGAGATTTCTTTGCATTAGCTCATCTTGAGCTCAG	301
Oy	266	CCCTGCGGAGAAAGGAGTCCGATTCTCTGCGGGGCTCTTAAAGGGAGTTTGTCTCT	325
Db	302	CTCTGTGGAGAAAGGAGTCCGATTCTCTGCGGGGCTCTTAAAGGGAGTTTGTCTCT	361
Oy	326	ACTGTGACAAGATTAAGGACAAAGTCATCCCTTCAGCTGAGAGAGAGAACTGA	385
Db	362	ACTGTGACAAGATTAAGGACAAAGTCATCCCTTCAGCTGAGAGAGAGAACTGA	421
Oy	386	TGAAGCTGGCTGCCAAAGGAATCAGCAGCGCGGCTTCATCTTTATGCGGCTCAGG	445
Db	422	TGAAGCTGGCTGCCAAAGGAATCAGCAGCGCGGCTTCATCTTTATGCGGCTCAGG	481
Oy	446	TGGAGCTCCGGAACATGCTGAGAGTGGGCGGCTCACCCCGAATGGTTCATCTGACCTCCT	505
Db	482	TGGAGCTCCGGAACATGCTGAGAGTGGGCGGCTCACCCCGAATGGTTCATCTGACCTCCT	541
Oy	506	GCAATTTGTAATGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACACTTGAAT	565
Db	542	GCAATTTGTAATGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACACTTGAAT	601
Oy	566	TTTTCATTTCACCAATTGGAAGCTGGAATGAGCCCACTGAGGTCAGCGATTGAG	621

Db 602 TTTCA TTTCA ACCAG TTTG CAAAG CTGA AATGA GCCCCAG TGAGGT CAGCG ATTAG 657

RESULT 3

```

US-09-398-412B-1
; Sequence 1, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-12eta, related reagen
; TITLE OF INVENTION: methods
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (491)..(1144)
; OTHER INFORMATION:
US-09-398-412B-1

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Query Match	78.5%	Score 510.4	DB 4	Length 1225
Best Local Similarity	97.9%	Pred. No. 8.1e-150		
Matches 517; Conservative	0	Mismatches 11	Indels 0	Gaps 0

OY	99	TCCTTGCAGAGGCTCCAAAGGTGAAGAACTTTAAACCCGAAAGAAATTCAGCTTCTATGACCA	158
Db	625	TGTTTCACACAGTGGAAAGGTGAAGAGCTTTAAACCCGAAAGAAATTCAGCTTCTATGACCA	684
OY	159	GGATTCACAAAGTACTGCTGCTCGTAGCTCGGGAATCTCATAGCAGTTCAGATPAAAACTA	218
Db	685	GGATTCACAAAGTACTGCTGCTCGTAGCTCGGGAATCTCATACAGTTCAGATPAAAACTA	744
OY	219	CATACGCCCAAGATTCCTTTTGCATTATAGCTCATCCTTGAGCTCAGCTCTGCGAGAA	278
Db	745	CATACGCCCAAGATTCCTTTTGCATTATAGCTCATCCTTGAGCTCAGCTCTGCGAGAA	804
OY	279	AGGAAGTCCGATTTCTCTCGGGGGGTCTCTAAAGGGAGTTTGTGTCTTACTGTGACAAAGA	338
Db	805	AGGAAGTCTGATTTCTCTCGGGGGGTCTCTAAAGGGAGTTTGTGTCTTACTGTGACAAAGA	864
OY	339	TAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGAGCTGGCTGC	398
Db	865	TAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGAGCTGGCTGC	924
OY	399	CCAAAGGAATCAGACACGCGCGCCCTTCATCTTTATATAGGAGCTCAGGTGGGCTCCTGAA	458
Db	925	CCAAAGGAATCAGACACGCGCGCCCTTCATCTTTATATAGGAGCTCAGGTGGGCTCCTGAA	984
OY	459	CATGCTGAGTCCGGCGGCTCACCCCGGATGGTTTATCTGCACTTCCTGCATTGTGAATGA	518
Db	985	CATGCTGAGTCCGGCGGCTCACCCCGGATGGTTTATCTGCACTTCCTGCAAATGTGAATGA	1044
OY	519	GCTGTGGGGGTGACAGATTAATTTTGGAAACAGGAAACACATTGAATTTTCATTTCACAC	578
Db	1045	GCTGTGGGGGTGACAGATTAATTTTGGAAACAGGAAACACATTGAATTTTCATTTCACAC	1104
OY	579	AGTTTGCACAAAGCTGAATGAGCCCCAGTGAAGCTCAGCGATTATAGGGTAC 626	
Db	1105	AGTTTGCACAAAGCTGAATGAGCCCCAGTGAAGCTCAGCGATTATAGGGAAAC 1152	

RESULT 4
US-09-128-155-1
; Sequence 1, Application US/09128155
; Patent No. 6117654

```

; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (356)...(889)
US-09-128-155-1

```

```

Query Match      61.1%; Score 397; DB 3; Length 989;
Best Local Similarity 97.6%; Pred. No. 36-114;
Matches 403; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 214 AACTACATACGCCGAGATCTTCTTGATAGGCTCCTTGAGCTCAGCTCTGCG 273
    |||
DB 485 AATTGTGTCACAAAAGATCTTCTTGATAGGCTCCTTGAGCTCAGCTCTGCG 544
    |||
QY 274 GAGAAAGGAAGTCCGATCTCTCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 333
    |||
DB 545 GAGAAAGGAAGTCCGATCTCTCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 604
    |||
QY 334 AAGGATAAGGACAAAGTCATCTCCTTCACTGAGGAGAGAACTGATGAAGCTG 393
    |||
DB 605 AAGGATAAGGACAAAGTCATCTCCTTCACTGAGGAGAGAACTGATGAAGCTG 664
    |||
QY 394 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGGCTCC 453
    |||
DB 665 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGGCTCC 724
    |||
QY 454 TGAACATGCTGAGTCCGCGGCTCACCOCGAGTGTTCATCTGACCTCTGCAATTGT 513
    |||
DB 725 TGAACATGCTGAGTCCGCGGCTCACCOCGAGTGTTCATCTGACCTCTGCAATTGT 784
    |||
QY 514 AATGAGCTGTGGGTGACAGATAATTGAGAACAGAAACACATTGAATTTTCATTT 573
    |||
DB 785 AATGAGCTGTGGGTGACAGATAATTGAGAACAGAAACACATTGAATTTTCATTT 844
    |||
QY 574 CAACGAGTTTGCAAGCTGAATATGAGCCGAGTGAGTCAAGGATTAAGGATAC 626
    |||
DB 845 CAACGAGTTTGCAAGCTGAATATGAGCCGAGTGAGTCAAGGATTAAGGATAC 897
    |||

```

RESULT 5
US-09-128-155-10

```

; Sequence 10, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10

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```

; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-09-128-155-10

```

```

Query Match      60.3%; Score 392.2; DB 3; Length 408;
Best Local Similarity 98.0%; Pred. No. 6.3e-113;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 214 AACTACATACGCCGAGATCTTCTTGATAGGCTCCTTGAGCTCAGCTCTGCG 273
    |||
DB 4 AATTGTGTCACAAAAGATCTTCTTGATAGGCTCCTTGAGCTCAGCTCTGCG 63
    |||
QY 274 GAGAAAGGAAGTCCGATCTCTCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 333
    |||
DB 64 GAGAAAGGAAGTCCGATCTCTCGGGGCTCTTAAAGGGAGTTTGTCTTACTGTGAC 123
    |||
QY 334 AAGGATAAGGACAAAGTCATCTCCTTCACTGAGGAGAGAACTGATGAAGCTG 393
    |||
DB 124 AAGGATAAGGACAAAGTCATCTCCTTCACTGAGGAGAGAACTGATGAAGCTG 183
    |||
QY 394 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGGCTCC 453
    |||
DB 184 GCTGCCCAAAAGGATCAGACGCGGCGCTTCATCTTTATAGGGCTCAGGTGAGGCTCC 243
    |||
QY 454 TGAACATGCTGAGTCCGCGGCTCACCOCGAGTGTTCATCTGACCTCTGCAATTGT 513
    |||
DB 244 TGAACATGCTGAGTCCGCGGCTCACCOCGAGTGTTCATCTGACCTCTGCAATTGT 303
    |||
QY 514 AATGAGCTGTGGGTGACAGATAATTGAGAACAGAAACACATTGAATTTTCATTT 573
    |||
DB 304 AATGAGCTGTGGGTGACAGATAATTGAGAACAGAAACACATTGAATTTTCATTT 363
    |||
QY 574 CAACGAGTTTGCAAGCTGAATATGAGCCGAGTGAGTCAAGGAT 618
    |||
DB 364 CAACGAGTTTGCAAGCTGAATATGAGCCGAGTGAGTCAAGGAT 408
    |||

```

RESULT 6
US-09-128-155-6

```

; Sequence 6, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(501)
US-09-128-155-6

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```

Query Match      60.3%; Score 392.2; DB 3; Length 501;
Best Local Similarity 98.0%; Pred. No. 6.9e-113;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 214 AACTACATACGCCGAGATCTTCTTGATAGGCTCCTTGAGCTCAGCTCTGCG 273
    |||

```

Db 97 AATTTGTTTCACACAAAGATCTTTCTTGATTAAGCTACTCTTGAGCTCAGCTCTGCG 156
Qy 274 GAGAAAGAGAGTCCGATTCCTCGGGGCTCTCTAAAGGGAGTTTGTCTACTGTGAC 333
Db 157 GAGAAAGAGAGTCCGATTCCTCGGGGCTCTCTAAAGGGAGTTTGTCTACTGTGAC 216
Qy 334 AAGGATTAAGGACAAAGTATCATCTCTTCACTGAGAGAGAGAACTGATGAAGCTG 393
Db 217 AAGGATTAAGGACAAAGTATCATCTCTTCACTGAGAGAGAACTGATGAAGCTG 276
Qy 394 GCTGCCCAAAAGAAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 453
Db 277 GCTGCCCAAAAGAAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 336
Qy 454 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGTTCATCTGACCTCTGCAATTTG 513
Db 337 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGTTCATCTGACCTCTGCAATTTG 396
Qy 514 AATGAGCTCTGGGTGACAGATAATTTGAGAACAGAAACACATTGAATTTTCATTT 573
Db 397 AATGAGCTCTGGGTGACAGATAATTTGAGAACAGAAACACATTGAATTTTCATTT 456
Qy 574 CAACGATTTGCAAGCTGAATGAGCCCGCAGTGAAGTCAAGGAT 618
Db 457 CAACGATTTGCAAGCTGAATGAGCCCGCAGTGAAGTCAAGGAT 501

RESULT 7
US-09-128-155-3

Sequence 3, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 534
TYPE: DNA
ORGANISM: Homo sapiens
US-09-128-155-3

Query Match 60.3%; Score 392.2; DB 3; Length 534;
Best Local Similarity 98.0%; Pred. No. 7,1e-113;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 214 AACTACATACGCGCCAGAGATCTTTCTTGATTAAGCTACTCTTGAAGTCAAGCTCTGCG 273
Db 130 AATTTGTTTCACACAAAGATCTTTCTTGATTAAGCTACTCTTGAAGTCAAGCTCTGCG 189
Qy 274 GAGAAAGAGAGTCCGATTCCTCGGGGCTCTCTAAAGGGAGTTTGTCTACTGTGAC 333
Db 190 GAGAAAGAGAGTCCGATTCCTCGGGGCTCTCTAAAGGGAGTTTGTCTACTGTGAC 249
Qy 334 AAGGATTAAGGACAAAGTATCATCTCTTCACTGAGAGAGAGAACTGATGAAGCTG 393
Db 250 AAGGATTAAGGACAAAGTATCATCTCTTCACTGAGAGAGAGAACTGATGAAGCTG 309
Qy 394 GCTGCCCAAAAGAAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 453
Db 310 GCTGCCCAAAAGAAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCC 369
Qy 454 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGTTCATCTGACCTCTGCAATTTG 513
Db 370 TGGAAATGCTGAGTGGCGGCTCAACCCGAGTGTTCATCTGACCTCTGCAATTTG 429

Qy 514 AATGAGCTCTGGGTGACAGATAATTTGAGAACAGGAAACACATTGAATTTTCATTT 573
Db 430 AATGAGCTCTGGGTGACAGATAATTTGAGAACAGGAAACACATTGAATTTTCATTT 489
Qy 574 CAACGATTTGCAAGCTGAATGAGCCCGCAGTGAAGTCAAGGAT 618
Db 490 CAACGATTTGCAAGCTGAATGAGCCCGCAGTGAAGTCAAGGAT 534

RESULT 8
US-09-128-155-17

Sequence 17, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 176373
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)...(176373)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 38.9%; Score 252.8; DB 3; Length 176373;
Best Local Similarity 99.2%; Pred. No. 7.5e-68;
Matches 254; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 371 AGAAGAGAAACTGATGAAGTGGTGGCCCAAAAGAAATGACACGCGGCTTCATCT 430
Db 158957 AGAAGAGAAACTGATGAAGTGGTGGCCCAAAAGAAATGACACGCGGCTTCATCT 159016
Qy 431 TTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGAGGCGGCTCACCCCGATGGT 490
Db 159017 TTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGAGGCGGCTCACCCCGATGGT 159076
Qy 491 TCATCTGACCTCTGCAATTTGTAATGAGCTGTTGGGTGACAGATAATTTGAGAAC 550
Db 159077 TCATCTGACCTCTGCAATTTGTAATGAGCTGTTGGGTGACAGATAATTTGAGAAC 159136
Qy 551 GGAACAACATTTGATTTTCATTTCAACCAAGTTTGCAAGCTGAATGAGCCCGCAGTGA 610
Db 159137 GGAACAACATTTGATTTTCATTTCAACCAAGTTTGCAAGCTGAATGAGCCCGCAGTGA 159196
Qy 611 TCAGGATTTAGGGTAC 626
Db 159197 TCAGGATTTAGGAAAC 159212

RESULT 9
US-08-330-638D-1

Sequence 1, Application US/08330638D
Patent No. 5731425
GENERAL INFORMATION:
APPLICANT: Brizzard, Billy
APPLICANT: Bianca, Darlene
APPLICANT: Chubet, Richard
APPLICANT: Wizard, Douglas
APPLICANT: Hopf, Thomas
TITLE OF INVENTION: POLYPEPTIDE SURFACE

TITLE OF INVENTION: MARKER FOR CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES: 10
ADDRESSER: Eastman Kodak Company,
ADDRESSER: Patent Legal Staff
STREET: 343 State Street
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14650-2201
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 MB storage, (Hewlett Packard)
COMPUTER: HP Vectra
OPERATING SYSTEM: MS-DOS Version 6.0
SOFTWARE: WORD FOR WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,638D
FILING DATE: 28 OCT 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
ATTORNEY/AGENT INFORMATION:
NAME: Kiernan, Anne B.
REGISTRATION NUMBER: 36,566
REFERENCE/DOCKET NUMBER: 71255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 588-2405
TELEFAX: (716) 477-4646
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: DOUBLE
TOPOLOGY: Linear
MOLECULE TYPE: SYNTHETIC GENE
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: SYNTHETICALLY PREPARED
IMMEDIATE SOURCE: SYNTHETICALLY PREPARED
FEATURE: SECRETION LEADER SEQUENCE
FEATURE: LOCATION: 1-45
FEATURE: FEATURE: CELL MARKER SEGMENT
FEATURE: LOCATION: 46-69
FEATURE: FEATURE: SPACER SEGMENT
FEATURE: LOCATION: 70-132
FEATURE: FEATURE: TRANSMEMBRANE SEGMENT
FEATURE: LOCATION: 133-195
FEATURE: FEATURE: ANCHOR SEGMENT
FEATURE: LOCATION: 196-204
PUBLICATION INFORMATION: NONE
US-08-330-638D-1

Query Match 10.6%; Score 69; DB 1; Length 204;
Best Local Similarity 100.0%; Pred.No. 1.4e-11;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGTCTGCACTTCTGATCTTGTGTGAGCTGCGAGTTCGACTACAAAGCAGT 69
DB 1 ATGTCTGCACTTCTGATCTTGTGTGAGCTGCGAGTTCGACTACAAAGCAGT 60

QY 70 GACGACAG 78
DB 61 GACGACAG 69

RESULT 10
US-08-906-746A-1
Sequence 1, Application US/08906746A
Patent No. 5945292
GENERAL INFORMATION:
APPLICANT: Brizzard, Billy L.
APPLICANT: Bianca, Darlene W.
APPLICANT: Chubert, Richard G.

APPLICANT: Vizard, Douglas L.
APPLICANT: Hopp, Thomas P.
TITLE OF INVENTION: Method of Identifying Cells with
TITLE OF INVENTION: Polypeptide Surface Marker
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES: 10
ADDRESSER: Semigier, Powers, Leavitt & Roedel
STREET: One Metropolitan Square- 16th Floor
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,746A
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Paul A.
REGISTRATION NUMBER: 38,628
REFERENCE/DOCKET NUMBER: SGM 6874
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-231-5400
TELEFAX: 314-231-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..45
OTHER INFORMATION: /function= "Secretion leader
FEATURE:
NAME/KEY: misc feature
LOCATION: 46..69
OTHER INFORMATION: /function= "Cell Marker Segment"
FEATURE:
NAME/KEY: misc feature
LOCATION: 70..132
OTHER INFORMATION: /function= "Spacer Segment"
FEATURE:
NAME/KEY: misc feature
LOCATION: 133..195
OTHER INFORMATION: /product= "Transmembrane Segment"
FEATURE:
NAME/KEY: misc feature
LOCATION: 196..204
OTHER INFORMATION: /product= "Anchor Segment"
US-08-906-746A-1

Query Match 10.6%; Score 69; DB 2; Length 204;
Best Local Similarity 100.0%; Pred.No. 1.4e-11;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ATGTCTGCACTTCTGATCTTGTGTGAGCTGCGAGTTCGACTACAAAGCAGT 69
DB 1 ATGTCTGCACTTCTGATCTTGTGTGAGCTGCGAGTTCGACTACAAAGCAGT 60

QY 70 GACGACAG 78
DB 61 GACGACAG 69

RESULT 11
US-08-644-271-31
; Sequence 31, Application US/08644271
; Patent No. 5814478
; GENERAL INFORMATION:
; APPLICANT: Valenzuela, et al.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS
; TITLE OF INVENTION: AND LIGANDS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,271
; FILING DATE: 10-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/008,657
; FILING DATE: 15-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: REG 195A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-345-7400
; TELEFAX: 914-345-7721
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1479 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1476
; OTHER INFORMATION:
; NAME/KEY: Human Agrin
; LOCATION: 1..1479
; OTHER INFORMATION:
US-08-644-271-31
Query Match 10.6%; Score 69; DB 1; Length 1479;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 ATGTCGACCTCTGATCTAGCTCTTGTGGAGCTGCGAGTTGCTGACTACAAAGACGAT 69
DB 1 ATGTCGACCTCTGATCTAGCTCTTGTGGAGCTGCGAGTTGCTGACTACAAAGACGAT 60
QY 70 GACGACAAG 78
DB 61 GACGACAAG 69
RESULT 12
US-09-077-955-35
; Sequence 35, Application US/09077955A
; Patent No. 6413740
; GENERAL INFORMATION:
; APPLICANT: Valenzuela et al., David M.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
; FILE REFERENCE: REG195-B-PCT-US

; CURRENT APPLICATION NUMBER: US/09/077,955A
; CURRENT FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: PCT/US96/20696
; EARLIER FILING DATE: 1996-12-13
; EARLIER APPLICATION NUMBER: 08/644,271
; EARLIER FILING DATE: 1996-05-10
; EARLIER APPLICATION NUMBER: 60/008,657
; EARLIER FILING DATE: 1995-12-15
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-077-955-35
Query Match 10.6%; Score 69; DB 3; Length 1479;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 ATGTCGACCTCTGATCTAGCTCTTGTGGAGCTGCGAGTTGCTGACTACAAAGACGAT 69
DB 1 ATGTCGACCTCTGATCTAGCTCTTGTGGAGCTGCGAGTTGCTGACTACAAAGACGAT 60
QY 70 GACGACAAG 78
DB 61 GACGACAAG 69
RESULT 13
US-07-977-451-7
; Sequence 7, Application US/07977451
; Patent No. 5270458
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 19921119
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US UNASSIGNED
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-977-451-7

Query Match 9.7%; Score 63.2; DB 1; Length 96;
Best Local Similarity 89.5%; Pred. No. 6.5e-10;
Matches 68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TCACCATGTCGACTTGTGATCTTAGCTCTTGTGGAGCTGCACTGCTGACTACAAG 64

Db 18 TCACCATGATGACATCTTGATCTTAGCCCTTGTGGAGCTCTGTGCTGACTACAAG 77

Qy 65 ACGATGACGACAACT 80
Db 78 ATGATGATGACAAAGAT 93

RESULT 14

US-08-252-517-7
Sequence 7, Application US/08252517
Patent No. 5548065
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,517
FILING DATE: 31-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-252-517-7

Query Match 9.7%; Score 63.2; DB 1; Length 96;
Best Local Similarity 89.5%; Pred. No. 6.5e-10;
Matches 68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TCACCATGTCGACTTGTGATCTTAGCTCTTGTGGAGCTGCACTGCTGACTACAAG 64

Db 18 TCACCATGATGACATCTTGATCTTAGCCCTTGTGGAGCTCTGTGCTGACTACAAG 77

Qy 65 ACGATGACGACAACT 80
Db 78 ATGATGATGACAAAGAT 93

RESULT 15

US-08-601-891-7
Sequence 7, Application US/08601891
Patent No. 5747651
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor R.
TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,891
FILING DATE: 15-FEB-1996

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,451
FILING DATE: 19-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/906,397
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/05401
FILING DATE: 26-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TW 81102961
FILING DATE: 15-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US92/02750
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,593
FILING DATE: 24-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,065
FILING DATE: 15-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,913
FILING DATE: 28-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/679,666
FILING DATE: 02-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEM-3-7P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEX: 212-645-2054
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-601-891-7

Query Match 9.7%; Score 63.2; DB 1; Length 96;
Best Local Similarity 89.5%; Pred. No. 6.5e-10;
Matches 68; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 TCACCATGCTGCACCTTCTAGCTCTGTTGAGCTGCAGTTCGCTGCTGACTACAAG 64
DB 18 TCACCATGAGTGCACCTTCTAGCTCTGCTTGGAGCTGCTGCTGACTACAAG 77
QY 65 ACGATGACGACAAGCT 80
DB 78 ATGATGATGACAAGAT 93

Search completed: May 28, 2005, 17:23:11
Job time : 163 secs

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OM nucleic - nucleic search, using SW model

Run on: May 28, 2005, 15:31:20 ; Search time 519 Seconds
(without alignments)
7689.236 Million cell updates/sec

Title: US-09-869-566-4

Perfect score: 650
Sequence: 1 taatcaccatgcctgcact.....cgactctagagatcccgag 650

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5700845 seqs, 306979757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516.8	79.5	802	9	US-09-788-963-1
2	516.8	79.5	1600	15	US-10-302-554-1
3	516	79.4	579	18	US-09-876-790-1
4	516	79.4	579	18	US-10-888-918-1
5	516	79.4	579	19	US-10-888-779-1
6	516	79.4	579	19	US-10-888-867-1
7	516	79.4	579	19	US-10-888-780-1
8	516	79.4	579	19	US-10-888-931-1
9	515.2	79.3	657	17	US-10-695-195-3
10	515.2	79.3	657	17	US-10-694-978-3
11	515	79.2	657	10	US-09-876-790-5

12	515	79.2	657	18	US-10-888-918-5	Sequence 5, Appli
13	515	79.2	657	19	US-10-888-779-5	Sequence 5, Appli
14	515	79.2	657	19	US-10-888-867-5	Sequence 5, Appli
15	515	79.2	657	19	US-10-888-780-5	Sequence 5, Appli
16	515	79.2	657	19	US-10-888-931-5	Sequence 5, Appli
17	514	79.1	594	10	US-09-876-790-6	Sequence 6, Appli
18	514	79.1	594	18	US-10-888-918-6	Sequence 6, Appli
19	514	79.1	594	19	US-10-888-779-6	Sequence 6, Appli
20	514	79.1	594	19	US-10-888-867-6	Sequence 6, Appli
21	514	79.1	594	19	US-10-888-780-6	Sequence 6, Appli
22	514	79.1	594	19	US-10-888-931-6	Sequence 6, Appli
23	513.6	79.0	630	9	US-09-965-528-51	Sequence 51, Appli
24	513.6	79.0	630	11	US-09-969-984-51	Sequence 51, Appli
25	513	78.9	657	15	US-10-302-554-13	Sequence 15, Appli
26	510.4	78.5	1225	17	US-10-695-195-1	Sequence 1, Appli
27	510.4	78.5	1225	17	US-10-694-978-1	Sequence 1, Appli
28	505.8	77.8	754	13	US-10-066-867-141	Sequence 141, App
29	505.8	77.8	754	13	US-10-063-547-141	Sequence 141, App
30	505.8	77.8	754	13	US-10-063-551-141	Sequence 141, App
31	505.8	77.8	754	14	US-10-063-616-141	Sequence 141, App
32	505.8	77.8	754	14	US-10-063-569-141	Sequence 141, App
33	505.8	77.8	754	14	US-10-063-513-141	Sequence 141, App
34	505.8	77.8	754	14	US-10-063-515-141	Sequence 141, App
35	505.8	77.8	754	14	US-10-063-512-141	Sequence 141, App
36	505.8	77.8	754	14	US-10-063-502-141	Sequence 141, App
37	505.8	77.8	754	14	US-10-063-549-141	Sequence 141, App
38	505.8	77.8	754	14	US-10-063-554-141	Sequence 141, App
39	505.8	77.8	754	14	US-10-063-553-141	Sequence 141, App
40	505.8	77.8	754	14	US-10-063-518-141	Sequence 141, App
41	505.8	77.8	754	14	US-10-063-598-141	Sequence 141, App
42	505.8	77.8	754	14	US-10-227-693-141	Sequence 141, App
43	505.8	77.8	754	14	US-10-063-563-141	Sequence 141, App
44	505.8	77.8	754	14	US-10-063-555-141	Sequence 141, App
45	505.8	77.8	754	14	US-10-063-594-141	Sequence 141, App

ALIGNMENTS

RESULT 1
US-09-788-963-1
; Sequence 1, Application US/09788963
; Patent No. US20020052473A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG, PETER R.
; APPLICANT: McDONNELL, PETER C.
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, MAT IL-1H4
; FILE REFERENCE: GP-70607-1C1
; CURRENT APPLICATION NUMBER: US/09/788,963
; PRIOR APPLICATION NUMBER: 09/293,625
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/452,140
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 802
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-788-963-1

Query Match 79.5%; Score 516.8; DB 9; Length 802;
Best Local Similarity 98.7%; Pred. No. 5.1e-162;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 99 TCTTGCAGAGTCCAAAGTGGAAGTAATTAACCCGAGAAATTCACATTCATGACCA 158
DB 192 TGTTCACCAAGTCCAAAGTGGAAGTAATTAACCCGAGAAATTCACATTCATGACCA 251
QY 159 GGATCACAAAGTACTGCTGCACTTGGGAATTCATACGATTCAGATTAATAAATCTA 218

Db 252 GGATCACAAGAGTCTGCTGCTGACTCTGGGAATCTCATAGCAATTGCAATTAATACTA 311
Qy 219 CATAGCCCAAGAGATCTTCTTGTGATTAAGCTCATCTTGAAGCTGAGCTCTGCGAGAA 278
Db 312 CATAGCCCAAGAGATCTTCTTGTGATTAAGCTCATCTTGAAGCTGAGCTCTGCGAGAA 371
Qy 279 AGGAAGTCGATCTCTGCGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGA 338
Db 372 AGGAAGTCGATCTCTGCGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGA 431
Qy 339 TAAAGACAAAGTCTATCCATCTCTTCAAGTGAAGAAAGAAATCGATGAAGCTGCTGC 398
Db 432 TAAAGACAAAGTCTATCCATCTCTTCAAGTGAAGAAAGAAATCGATGAAGCTGCTGC 491
Qy 399 CCAAGAGATCAGACAGCCGCGCTCTCATCTTTATAGAGGCTCAGTGGGCTCCTGGA 458
Db 492 CCAAGAGATCAGACAGCCGCGCTCTCATCTTTATAGAGGCTCAGTGGGCTCCTGGA 551
Qy 459 CATGCTGAGTCGCGGGCTCACCCCGATGTTCAITCTGCACTCTGCAATTTGTAATGA 518
Db 552 CATGCTGAGTCGCGGGCTCACCCCGATGTTCAITCTGCACTCTGCAATTTGTAATGA 611
Qy 519 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCAATTTCAAC 578
Db 612 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCAATTTCAAC 671
Qy 579 AGTTGCAAGCTGAATGAGCCCGATGAGGTGAGCGATTAGGGTAC 626
Db 672 AGTTGCAAGCTGAATGAGCCCGATGAGGTGAGCGATTAGGGTAC 719

RESULT 2
US-10-302-554-1
Sequence 1, Application US/10302554
Publication No. US20030148467A1

GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Shepard, Paul O.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
FILE REFERENCE: 98-59
CURRENT APPLICATION NUMBER: US/10/302,554
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/428,118
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: US 60/105,824
PRIOR FILING DATE: 1998-10-27
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1600
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (847) ... (1503)
US-10-302-554-1

Query Match 79.5%; Score 516.8; DB 15; Length 1600;
Best Local Similarity 98.7%; Pred. No. 7.3e-162;
Matches 521; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db 981 TCTTTCACACAGTCCAAAGGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACCA 1040
Qy 159 GGATCACAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAAGTTCAGATTAATACTA 218
Db 1041 GGATCACAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAAGTTCAGATTAATACTA 1100
Qy 219 CATAGCCCAAGAGATCTTCTTGTGATTAAGCTCATCTTGAAGCTGAGCTCTGCGAGAA 278
Db 1101 CATAGCCCAAGAGATCTTCTTGTGATTAAGCTCATCTTGAAGCTGAGCTCTGCGAGAA 1160

Qy 279 AGGAAGTCGATCTCTGCGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGA 338
Db 1161 AGGAAGTCGATCTCTGCGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGA 1220
Qy 339 TAAAGACAAAGTCTATCCATCTCTTCAAGTGAAGAAAGAAATCGATGAAGCTGCTGC 398
Db 1221 TAAAGACAAAGTCTATCCATCTCTTCAAGTGAAGAAAGAAATCGATGAAGCTGCTGC 1280
Qy 399 CCAAGAGATCAGACAGCCGCGCTCTCATCTTTATAGAGGCTCAGTGGGCTCCTGGA 458
Db 1281 CCAAGAGATCAGACAGCCGCGCTCTCATCTTTATAGAGGCTCAGTGGGCTCCTGGA 1340
Qy 459 CATGCTGAGTCGCGGGCTCACCCCGATGTTCAITCTGCACTCTGCAATTTGTAATGA 518
Db 1341 CATGCTGAGTCGCGGGCTCACCCCGATGTTCAITCTGCACTCTGCAATTTGTAATGA 1400
Qy 519 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCAATTTCAAC 578
Db 1401 GCTGTGGGGTGACAGATTAATTTGAGAACAGAAACATTTGATTTTCAATTTCAAC 1460
Qy 579 AGTTGCAAGCTGAATGAGCCCGATGAGGTGAGCGATTAGGGTAC 626
Db 1461 AGTTGCAAGCTGAATGAGCCCGATGAGGTGAGCGATTAGGGTAC 1508

RESULT 3
US-09-876-790-1
Sequence 1, Application US/09876790
Publication No. US20030091532A1

GENERAL INFORMATION:
APPLICANT: SIMS, John E.
APPLICANT: SMITH, Dirk E.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRECD DNAS AND POLYPEPTID
FILE REFERENCE: 2008-US
CURRENT APPLICATION NUMBER: US/09/876,790
CURRENT FILING DATE: 2002-09-04
PRIOR APPLICATION NUMBER: 60/112,163
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/146,675
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/29549
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 579
TYPE: DNA
ORGANISM: Homo sapiens
US-09-876-790-1

Query Match 79.4%; Score 516; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 7.9e-162;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 106 AGAGGTCCAAAGGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACCAAGATCAC 165
Db 64 AGAGGTCCAAAGGTGAAGAACTTAACCCGAAGAAATTCAGATTCATGACCAAGATCAC 123
Qy 166 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAAGTTCAGATTAATACTACATACGC 225
Db 124 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAAGTTCAGATTAATACTACATACGC 183
Qy 226 CCAAGATCTTCTTGTGATTAAGCTCATCTTGAAGCTCAGCTCTGCGAGAAAGAGT 285
Db 184 CCAAGATCTTCTTGTGATTAAGCTCATCTTGAAGCTCAGCTCTGCGAGAAAGAGT 243
Qy 286 CCGATTCCTCGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGGA 345
Db 244 CCGATTCCTCGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAAGATTAAGGA 303
Qy 346 CAAAGTATCATCTCTTCAAGTGAAGAAAGAACTGATGAAGCTGCTGCCCAAG 405

Db 304 CAAAGTCATCCATCCCTTCACTGAGGAAAGGAACTCATGAGCTGCTGCCAAAAG 363
Qy 406 GAATGAGCAGCGCGGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 465
Db 364 GAATGAGCAGCGCGGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 423
Qy 466 GAGTGGGCGGCTCACCGCGGATGTTCACTGCACTCTGCAATTGTATAGGCTGTT 525
Db 424 GAGTGGGCGGCTCACCGCGGATGTTCACTGCACTCTGCAATTGTATAGGCTGTT 483
Qy 526 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 585
Db 484 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 543
Qy 586 AAAGCTGAAATGAGCCCGCAGTGAAGTCAAGCATTAAG 621
Db 544 AAAGCTGAAATGAGCCCGCAGTGAAGTCAAGCATTAAG 579

RESULT 4

US-10-888-918-1
; Sequence 1, Application US/10888918
; Publication No. US20040248187A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,918
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-918-1

Query Match 79.4%; Score 516; DB 18; Length 579;
Best Local Similarity 100.0%; Pred. No. 7.9e-162; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0;

Qy 106 AGAGTCCAAAGGTGAAGAACTTAACCCGAAAGAAATTCAGATTCATGACGAGATCAC 165
Db 64 AGAGTCCAAAGGTGAAGAACTTAACCCGAAAGAAATTCAGATTCATGACGAGATCAC 123
Qy 166 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCACTTCCAGATTAATAAATCAATACGC 225
Db 124 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCACTTCCAGATTAATAAATCAATACGC 183
Qy 226 CCAGAGATCTTCTTTCATTAAGGAGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 285
Db 184 CCAGAGATCTTCTTTCATTAAGGAGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 243
Qy 286 CCGATTCCTCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 345
Db 244 CCGATTCCTCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 303
Qy 346 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAAAGTATGATGAGTGGCTGCCAAAAG 405
Db 304 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAAAGTATGATGAGTGGCTGCCAAAAG 363
Qy 406 GAATGAGCAGCGCGGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 465

Db 364 GAATGAGCAGCGCGGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 423
Qy 466 GAGTGGGCGGCTCACCGCGGATGTTCACTGCACTCTGCAATTGTATAGGCTGTT 525
Db 424 GAGTGGGCGGCTCACCGCGGATGTTCACTGCACTCTGCAATTGTATAGGCTGTT 483
Qy 526 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 585
Db 484 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 543
Qy 586 AAAGCTGAAATGAGCCCGCAGTGAAGTCAAGCATTAAG 621
Db 544 AAAGCTGAAATGAGCCCGCAGTGAAGTCAAGCATTAAG 579

RESULT 5

US-10-888-779-1
; Sequence 1, Application US/10888779
; Publication No. US20050009138A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICER VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,779
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-779-1

Query Match 79.4%; Score 516; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 7.9e-162; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0;

Qy 106 AGAGTCCAAAGGTGAAGAACTTAACCCGAAAGAAATTCAGATTCATGACGAGATCAC 165
Db 64 AGAGTCCAAAGGTGAAGAACTTAACCCGAAAGAAATTCAGATTCATGACGAGATCAC 123
Qy 166 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCACTTCCAGATTAATAAATCAATACGC 225
Db 124 AAAGTACTGCTCTGAGCTCTGGGAATCTCATAGCACTTCCAGATTAATAAATCAATACGC 183
Qy 226 CCAGAGATCTTCTTTCATTAAGGAGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 285
Db 184 CCAGAGATCTTCTTTCATTAAGGAGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 243
Qy 286 CCGATTCCTCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 345
Db 244 CCGATTCCTCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAGAGATAAGGA 303
Qy 346 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAAAGTATGATGAGTGGCTGCCAAAAG 405
Db 304 CAAAGTCATCCATCCCTTCACTGAGTGAAGAGAAAGTATGATGAGTGGCTGCCAAAAG 363
Qy 406 GAATGAGCAGCGCGGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 465
Db 364 GAATGAGCAGCGCGGCTTCACTTTTATAGGGCTCAGGTGGGCTCCGGAACATGCTG 423
Qy 466 GAGTGGGCGGCTCACCGCGGATGTTCACTGCACTCTGCAATTGTATAGGCTGTT 525

Db 424 GAGTGGCGGCTCACCCCGAGTGTCTCATCTGCACTCTGCAATTTGATAGAGCTGTT 483
QY 536 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 585
Db 484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 543
QY 586 AAAGCTGAAATAGAGCCCGCAGTGAAGTCAAGCATTTAG 621
Db 544 AAAGCTGAAATAGAGCCCGCAGTGAAGTCAAGCATTTAG 579

RESULT 6
US-10-888-867-1
; Sequence 1, Application US/10888867
; Publication No. US2005009075A1
; GENERAL INFORMATION:
; APPLICANT: STMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,867
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-867-1

Query Match 79.4%; Score 516; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 7.9e-162; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0;
QY 106 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACAGATCAC 165
Db 64 AAGGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACAGATCAC 123
QY 166 AAAGTACTGTCTCTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 225
Db 124 AAAGTACTGTCTCTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 183
QY 226 CCAAGATCTTCTTTCATTTAGCTTCATGCTGAGCTGAGCTGCGGAGAAAGAAAT 285
Db 184 CCAAGATCTTCTTTCATTTAGCTTCATGCTGAGCTGAGCTGCGGAGAAAGAAAT 243
QY 286 CCGATTCCTCTGGGGGTCTCTAAAGGGAGATTCTCTACTGTCAGAGATTAAGGA 345
Db 244 CCGATTCCTCTGGGGGTCTCTAAAGGGAGATTCTCTACTGTCAGAGATTAAGGA 303
QY 346 CAAAGTATCATCCCTTCAGCTGAAGAAAGAAATGATGAAGTGGCTGCCCAAAAG 405
Db 304 CAAAGTATCATCCCTTCAGCTGAAGAAAGAAATGATGAAGTGGCTGCCCAAAAG 363
QY 406 GAATCAGACGCGCGGCTCTTATTTAGGGCTCAGGTGGCTCTCTGAAACATGCTG 465
Db 364 GAATCAGACGCGCGGCTCTTATTTAGGGCTCAGGTGGCTCTCTGAAACATGCTG 423
QY 466 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGATAGAGCTGTT 525
Db 424 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGATAGAGCTGTT 483
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 585
Db 586 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 543

Db 484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 543
QY 586 AAAGCTGAAATAGAGCCCGCAGTGAAGTCAAGCATTTAG 621
Db 544 AAAGCTGAAATAGAGCCCGCAGTGAAGTCAAGCATTTAG 579

RESULT 7
US-10-888-780-1
; Sequence 1, Application US/10888780
; Publication No. US20050013797A1
; GENERAL INFORMATION:
; APPLICANT: STMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,780
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-780-1

Query Match 79.4%; Score 516; DB 19; Length 579;
Best Local Similarity 100.0%; Pred. No. 7.9e-162; Indels 0; Gaps 0;
Matches 516; Conservative 0; Mismatches 0;
QY 106 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACAGATCAC 165
Db 64 AAGGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACAGATCAC 123
QY 166 AAAGTACTGTCTCTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 225
Db 124 AAAGTACTGTCTCTGACTCTGGAATCTCATGACAGTTCCAGATTAATACTACATACGC 183
QY 226 CCAAGATCTTCTTTCATTTAGCTTCATGCTGAGCTGAGCTGCGGAGAAAGAAAT 285
Db 184 CCAAGATCTTCTTTCATTTAGCTTCATGCTGAGCTGAGCTGCGGAGAAAGAAAT 243
QY 286 CCGATTCCTCTGGGGGTCTCTAAAGGGAGATTCTCTACTGTCAGAGATTAAGGA 345
Db 244 CCGATTCCTCTGGGGGTCTCTAAAGGGAGATTCTCTACTGTCAGAGATTAAGGA 303
QY 346 CAAAGTATCATCCCTTCAGCTGAAGAAAGAAATGATGAAGTGGCTGCCCAAAAG 405
Db 304 CAAAGTATCATCCCTTCAGCTGAAGAAAGAAATGATGAAGTGGCTGCCCAAAAG 363
QY 406 GAATCAGACGCGCGGCTCTTATTTAGGGCTCAGGTGGCTCTCTGAAACATGCTG 465
Db 364 GAATCAGACGCGCGGCTCTTATTTAGGGCTCAGGTGGCTCTCTGAAACATGCTG 423
QY 466 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGATAGAGCTGTT 525
Db 424 GAGTGGGGGCTCACCCCGAGATGTTTCATCTGCACTCTGCAATTTGATAGAGCTGTT 483
QY 526 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 585
Db 484 GGGGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTTCACAGATTTC 543
QY 586 AAAGCTGAAATAGAGCCCGCAGTGAAGTCAAGCATTTAG 621

Db 544 AAAGTGAATGATGCCCCAGTGCAGGATTAAG 579

RESULT 8

US-10-888-931-1
; Sequence 1, Application US/10888931
; Publication No. US20050013798A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICE VARIANTS AND XRE2 DNAS AND POLYPEPT
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,931
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 1
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-931-1

Query Match 79.4%; Score 516; DB 19; Length 579;

Best Local Similarity 100.0%; Pred. No. 7.9e-162; Mismatches 0; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

106 AGAGTCCAAAGGTGAAGACTTAAACCCGAGAAATTCAGATTCATGACAGATCAC 165
64 AGAGTCCAAAGGTGAAGACTTAAACCCGAGAAATTCAGATTCATGACAGATCAC 123
166 AAAGTCTGCTCTGAGCTCTGGAATCTCATAGAGTTCCAGATTAATACTACATACGC 225
124 AAAGTCTGCTCTGAGCTCTGGAATCTCATAGAGTTCCAGATTAATACTACATACGC 183
226 CCAGAGATTTCTTTGATTAAGCTTCACTTCACTGAGCTCTGCGGAGAAAGAGT 285
184 CCAGAGATTTCTTTGATTAAGCTTCACTTCACTGAGCTCTGCGGAGAAAGAGT 243
286 CCAGATTTCTGAGGAGTCTTAAAGGAGATTTGCTCTCACTGAGCAAGATTAAGA 345
244 CCAGATTTCTGAGGAGTCTTAAAGGAGATTTGCTCTCACTGAGCAAGATTAAGA 303
346 CAAAGTCATCATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGCCAAAG 405
304 CAAAGTCATCATCCCTTCAGCTGAAGAGAACTGATGAAGCTGCTGCCAAAG 363
406 GAATCAGACGCGCGCTTCACTTTTATAGGCTCTGAGTGGGCTCTGGAACATGCTG 465
364 GAATCAGACGCGCGCTTCACTTTTATAGGCTCTGAGTGGGCTCTGGAACATGCTG 423
466 GAGTGGGAGGCTCACCCGGATGCTCATGCACTCTGCAATGTATAGAGCTGTT 525
424 GAGTGGGAGGCTCACCCGGATGCTCATGCACTCTGCAATGTATAGAGCTGTT 483
526 GGGGTGACAGATTAATTTGAGAACAGAAACATGAATTTTCATTTCAACAGTTTC 585
484 GGGGTGACAGATTAATTTGAGAACAGAAACATGAATTTTCATTTCAACAGTTTC 543
586 AAAGCTGAATAGAGCCCGAGTGAAGCTCAGGATTAAG 621
544 AAAGCTGAATAGAGCCCGAGTGAAGCTCAGGATTAAG 579

RESULT 9

US-10-695-195-3
; Sequence 3, Application US/10695195
; Publication No. US20040068099A1
; GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/695,195
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/398,412
FILING DATE: 17-Sep-1999

ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 657 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 1..654
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-695-195-3

Query Match 79.3%; Score 515.2; DB 17; Length 657;

Best Local Similarity 97.6%; Pred. No. 1.6e-161; Mismatches 13; Indels 0; Gaps 0;

Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

86 CCGGAAATTCAGCTCTTTCAGAGGTCCAAAGGTGAAGACTTAAACCCGAGAAATTC 145
122 CCGCATGAATTTTGTTCACAAAGTCCAAAGGTGAAGACTTAAACCCGAGAAATTC 181
146 GCATTCATGACAGATCAAAAGTACTGCTCTGAGCTCTGGGAATCTCATAGAGTTT 205
182 GCATTCATGACAGATCAAAAGTACTGCTCTGAGCTCTGGGAATCTCATAGAGTTT 241
206 CAGATTAATACTACATGAGCCAGAGATCTTTTCATTAAGCTTCATCTTGAAGCTG 265
242 CAGATTAATACTACATGAGCCAGAGATCTTTTCATTAAGCTTCATCTTGAAGCTG 301
266 CCTTCGCGAGAAAGAGTCCGATTTCTCTGAGGAGTCTTAAAGGAGATTTTGTCTCT 325
302 CCTTCGCGAGAAAGAGTCCGATTTCTCTGAGGAGTCTTAAAGGAGATTTTGTCTCT 361
326 ACTGTGACAGATTAAGAGCAAGATCATCTCTTCACTGAGTTGAAGAGAACTGA 385
362 ACTGTGACAGATTAAGAGCAAGATCATCTCTTCACTGAGTTGAAGAGAACTGA 421
386 TGAAGCTGAGTCCCAAAAGAAATCAGACGCGGAGCTTCACTTTTATAGGAGCTCAG 445

Db 422 TGAAGCTGGCTGCCAAAAGAAATGACACGCCGCCCTTCACTTTATATAGGCTCAGG 481
Qy 446 TGGGCTCCTGGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGCACTCCT 505
Db 482 TGGGCTCCTGGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGCACTCCT 541
Qy 506 GCAATTTGATATAGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACATTTGAAT 565
Db 542 GCAATTTGATATAGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACATTTGAAT 601
Qy 566 TTTCAATTTCAACAGCTTTGCAAAAGCTGAATAGAGCCCGAGTGGGTGAGGATTTAG 621
Db 602 TTTCAATTTCAACAGCTTTGCAAAAGCTGAATAGAGCCCGAGTGGGTGAGGATTTAG 657

RESULT 10

US-10-694-978-3

Sequence 3, Application US/10694978
Publication No. US20040087766A1
GENERAL INFORMATION:

APPLICANT: Timans, Jacqueline C.
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/694,978
APPLICATION NUMBER: US/10/694,978
FILING DATE: 27-Oct-2003
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/398,412

FILING DATE: 17-Sep-1999

ATTORNEY/AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0904K

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 852-9196

TELEFAX: (650) 496-1200

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 657 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..654

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-694-978-3

Query Match 79.3%; Score 515.2; DB 17; Length 657;
Best Local Similarity 97.6%; Pred. No. 1.6e-161;
Matches 523; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 86 CCGCGAATTCAGCTCTTTCAGAGGTCGCAAGGTGAAGACTTAAACCGGAAGAAATTCA 145
Db 122 CCGCGAATTCAGCTCTTTCAGAGGTCGCAAGGTGAAGACTTAAACCGGAAGAAATTCA 181
Qy 146 GCAATTCATGACAGATCAAGAGTACTGCTCTGAGCTCTGGAGTCTCATAGCAGTTG 205
Db 182 GCAATTCATGACAGATCAAGAGTACTGCTCTGAGCTCTGGAGTCTCATAGCAGTTG 241

Qy 206 CAGATTAATACTAATACAGCCGAGAGATCTTCTTTGCAATTAAGCTTCATCTTGAAGCTCAG 265
Db 242 CAGATTAATACTAATACAGCCGAGAGATCTTCTTTGCAATTAAGCTTCATCTTGAAGCTCAG 301
Qy 266 CCTCTGCGGAGAAAGAGATCCGATTTCTCTGCGGGGCTCTTAAAGGGAGTTTGTCT 325
Db 302 CCTCTGCGGAGAAAGAGATCCGATTTCTCTGCGGGGCTCTTAAAGGGAGTTTGTCT 361
Qy 326 ACTGTGACAGAGATTAAGGACAAAGTCAATCCCTTCAGCTGAGAGAGAGAAATGCA 385
Db 362 ACTGTGACAGAGATTAAGGACAAAGTCAATCCCTTCAGCTGAGAGAGAGAAATGCA 421
Qy 386 TGAAGCTGGCTGCCAAAAGAAATGACACGCCGCCCTTCACTTTTATAGGCTCAGG 445
Db 422 TGAAGCTGGCTGCCAAAAGAAATGACACGCCGCCCTTCACTTTTATAGGCTCAGG 481
Qy 446 TGGGCTCCTGGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGCACTCCT 505
Db 482 TGGGCTCCTGGAACAATGCTGAGTGGCGCGCTCACCCCGAATGTTCACTGCACTCCT 541
Qy 506 GCAATTTGATATAGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACATTTGAAT 565
Db 542 GCAATTTGATATAGAGCTGTTGGGGGTGACAGATTAATTTGAGAACAGAAACATTTGAAT 601
Qy 566 TTTCAATTTCAACAGCTTTGCAAAAGCTGAATAGAGCCCGAGTGGGTGAGGATTTAG 621
Db 602 TTTCAATTTCAACAGCTTTGCAAAAGCTGAATAGAGCCCGAGTGGGTGAGGATTTAG 657

RESULT 11

US-09-876-790-5

Sequence 5, Application US/09876790
Publication No. US20030091532A1
GENERAL INFORMATION:

APPLICANT: SIMS, John E.

APPLICANT: SMITH, Dirk E.

TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND KREC2 DNAS AND POLYPEPTIDES

FILE REFERENCE: 2008-US

CURRENT APPLICATION NUMBER: US/09/876,790

CURRENT FILING DATE: 2002-09-04

PRIOR FILING DATE: 1998-12-14

PRIOR APPLICATION NUMBER: 60/146,675

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: PCT/US99/29549

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5

LENGTH: 657

TYPE: DNA

ORGANISM: Homo sapiens

US-09-876-790-5

Query Match 79.2%; Score 515; DB 10; Length 657;
Best Local Similarity 99.0%; Pred. No. 1.8e-161;
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 99 TCTTTCAGAGGTCGCAAGGTGAAGACTTAAACCGGAAGAAATTCAGATTCATGACCA 158
Db 135 TCTTTCAGAGGTCGCAAGGTGAAGACTTAAACCGGAAGAAATTCAGATTCATGACCA 194
Qy 159 GATATCAAGAGTACGTCCTGAGCTCTGGAGATCTCATAGAGTTCAGATTAATACTA 218
Db 195 GATATCAAGAGTACGTCCTGAGCTCTGGAGATCTCATAGAGTTCAGATTAATACTA 254
Qy 219 CATAGCCCAAGAGATCTTCTTTCAGATTAAGCTCATCTTGAAGCTCAGCCTCTGCGAGAA 278
Db 255 CATAGCCCAAGAGATCTTCTTTCAGATTAAGCTCATCTTGAAGCTCAGCCTCTGCGAGAA 314
Qy 279 AGAAGTCGATTCCTCTGCGGGGCTCTTAAAGGGAAGTTTGTCTCTACTGTGACAAAGA 338

DB 315 AGAAGTCGATTCCTCTGAGGCTCTCTAAGGGAGTTTGTCTACTGACAAAGA 374
QY 339 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGAGAAACATGAGAGCTGCTGC 398
DB 375 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGAGAAACATGAGAGCTGCTGC 434
QY 399 CCAAAAGGATGACAGACGCGGCTTCTTATTAAGGCTCAGTGGGCTCTCGAA 458
DB 435 CCAAAAGGATGACAGACGCGGCTTCTTATTAAGGCTCAGTGGGCTCTCGAA 494
QY 459 CATGCTGAGTGGGCTCAGACCCCGAGTGTTCATCTGCACTCTGCAATTGATGA 518
DB 495 CATGCTGAGTGGGCTCAGACCCCGAGTGTTCATCTGCACTCTGCAATTGATGA 554
QY 519 GCCTGTTGGGGTGACAGATAAATTGAGAACGAGAAACATTGAATTTTCAATTCAC 578
DB 555 GCCTGTTGGGGTGACAGATAAATTGAGAACGAGAAACATTGAATTTTCAATTCAC 614
QY 579 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 621
DB 615 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 657

RESULT 12

US-10-888-918-5
; Sequence 5, Application US/10888918
; Publication No. US20040248187A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888, 918
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876, 790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146, 675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-918-5

Query Match 79.2%; Score 515; DB 18; Length 657;
Best Local Similarity 99.0%; Pred. No. 1.8e-161;
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGCAAGAGTCCAAAGTGAAGACTTAAACCCGAAAGAAATTGAGATTCATGACCA 158
DB 135 TCTTTGCAAGAGTCCAAAGTGAAGACTTAAACCCGAAAGAAATTGAGATTCATGACCA 194
QY 159 GGATCACAAAGTACTGCTCTGAGACTCTGGAAATCTCATAGAGTCCAGATTAATACTA 218
DB 195 GGATCACAAAGTACTGCTCTGAGACTCTGGAAATCTCATAGAGTCCAGATTAATACTA 254
QY 219 CATAGCCCAAGAGATCTTCTTGAATTAAGCTCATCTGAGCTCAGCTCTGCGAGAA 278
DB 255 CATAGCCCAAGAGATCTTCTTGAATTAAGCTCATCTGAGCTCAGCTCTGCGAGAA 314
QY 279 AGGAAGTCGATTCCTCTGAGGCTCTCTAAAGGGAGTTTGTCTTACTGTGACAAAGA 338
DB 315 AGGAAGTCGATTCCTCTGAGGCTCTCTAAAGGGAGTTTGTCTTACTGTGACAAAGA 374
QY 339 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGAGAAACATGAGAGCTGCTGC 398

DB 375 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGAGAAACATGAGAGCTGCTGC 434
QY 399 CCAAAAGGATGACAGACGCGGCTTCTTATTAAGGCTCAGTGGGCTCTCGAA 458
DB 435 CCAAAAGGATGACAGACGCGGCTTCTTATTAAGGCTCAGTGGGCTCTCGAA 494
QY 459 CATGCTGAGTGGGCTCAGACCCCGAGTGTTCATCTGCACTCTGCAATTGATGA 518
DB 495 CATGCTGAGTGGGCTCAGACCCCGAGTGTTCATCTGCACTCTGCAATTGATGA 554
QY 519 GCCTGTTGGGGTGACAGATAAATTGAGAACGAGAAACATTGAATTTTCAATTCAC 578
DB 555 GCCTGTTGGGGTGACAGATAAATTGAGAACGAGAAACATTGAATTTTCAATTCAC 614
QY 579 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 621
DB 615 AGTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 657

RESULT 13

US-10-888-779-5
; Sequence 5, Application US/10888779
; Publication No. US2005009138A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888, 779
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876, 790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146, 675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-779-5

Query Match 79.2%; Score 515; DB 19; Length 657;
Best Local Similarity 99.0%; Pred. No. 1.8e-161;
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGCAAGAGTCCAAAGTGAAGACTTAAACCCGAAAGAAATTGAGATTCATGACCA 158
DB 135 TCTTTGCAAGAGTCCAAAGTGAAGACTTAAACCCGAAAGAAATTGAGATTCATGACCA 194
QY 159 GGATCACAAAGTACTGCTCTGAGACTCTGGAAATCTCATAGAGTCCAGATTAATACTA 218
DB 195 GGATCACAAAGTACTGCTCTGAGACTCTGGAAATCTCATAGAGTCCAGATTAATACTA 254
QY 219 CATAGCCCAAGAGATCTTCTTGAATTAAGCTCATCTGAGCTCAGCTCTGCGAGAA 278
DB 255 CATAGCCCAAGAGATCTTCTTGAATTAAGCTCATCTGAGCTCAGCTCTGCGAGAA 314
QY 279 AGGAAGTCGATTCCTCTGAGGCTCTCTAAAGGGAGTTTGTCTTACTGTGACAAAGA 338
DB 315 AGGAAGTCGATTCCTCTGAGGCTCTCTAAAGGGAGTTTGTCTTACTGTGACAAAGA 374
QY 339 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGAGAAACATGAGAGCTGCTGC 398
DB 375 TAAAGGACAAAGTCATCCATCCCTTCAAGTGAAGAGAAACATGAGAGCTGCTGC 434
QY 399 CCAAAAGGATGACAGACGCGGCTTCTTATTAAGGCTCAGTGGGCTCTCGAA 458

DB 435 CCAAAAGGATGACGCGCGGCTTCACTTTTATAGGGCTCAGGTGGCTCCCGGAA 494
QY CATGCTGAGTGGGGGCTCACCCCGGAGTTCATCTGACACCTCCGCAATTTGTAATGA 518
DB 495 CATGCTGAGTGGGGGCTCACCCCGGAGTTCATCTGACACCTCCGCAATTTGTAATGA 554
QY 519 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAAC 578
DB 555 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAAC 614
QY 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 621
DB 615 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 657

RESULT 14

US-10-888-867-5
; Sequence 5, Application US/1088867
; Publication No. US2005009075A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,867
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-867-5

Query Match 79.2%; Score 515; DB 19; Length 657;
Best Local Similarity 99.0%; Pred. No. 1.8e-161;
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 158
DB 135 TCTTCAACAAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 194
QY 159 GGATCACAAAGTACTGCTCTGGAATCTGAGATCTGATGAGTTCGATTAATACTA 218
DB 195 GGATCACAAAGTACTGCTCTGGAATCTGAGATCTGATGAGTTCGATTAATACTA 254
QY 219 CATACGCCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGCTCAGCTTCGCGAGA 278
DB 255 CATACGCCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGCTCAGCTTCGCGAGA 314
QY 279 AGGAAGTCCGATTCCTGCGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGA 338
DB 315 AGGAAGTCCGATTCCTGCGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGA 374
QY 339 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAACTGATGAGTGGCTGC 398
DB 375 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAACTGATGAGTGGCTGC 434
QY 399 CCAAAAGGATGACGCGCGGCTTCACTTTTATAGGGCTCAGGTGGCTCCCGGAA 458
DB 435 CCAAAAGGATGACGCGCGGCTTCACTTTTATAGGGCTCAGGTGGCTCCCGGAA 494
QY 459 CATGCTGAGTGGGGGCTCACCCCGGAGTTCATCTGACACCTCCGCAATTTGTAATGA 518

DB 495 CATGCTGAGTGGGGGCTCACCCCGGAGTTCATCTGACACCTCCGCAATTTGTAATGA 554
QY 519 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAAC 578
DB 555 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAAC 614
QY 579 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 621
DB 615 AGTTTGCAAAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTTAG 657

RESULT 15

US-10-888-780-5
; Sequence 5, Application US/10888780
; Publication No. US20050013797A1
; GENERAL INFORMATION:
; APPLICANT: SIMS, John E.
; APPLICANT: SMITH, Dirk E.
; APPLICANT: BORN, Teresa L.
; TITLE OF INVENTION: IL-1 ZETA, IL-1 ZETA SPLICED VARIANTS AND XRE2 DNAS AND POLYPEPTI
; FILE REFERENCE: 2008-US
; CURRENT APPLICATION NUMBER: US/10/888,780
; PRIOR FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US/09/876,790
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/112,163
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/146,675
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: PCT/US99/29549
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-888-780-5

Query Match 79.2%; Score 515; DB 19; Length 657;
Best Local Similarity 99.0%; Pred. No. 1.8e-161;
Matches 518; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 99 TCTTTGACAGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 158
DB 135 TCTTCAACAAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCA 194
QY 159 GGATCACAAAGTACTGCTCTGGAATCTGAGATCTGATGAGTTCGATTAATACTA 218
DB 195 GGATCACAAAGTACTGCTCTGGAATCTGAGATCTGATGAGTTCGATTAATACTA 254
QY 219 CATACGCCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGCTCAGCTTCGCGAGA 278
DB 255 CATACGCCAGAGATCTTCTTTCATTTAGCTCATCTTGAAGCTCAGCTTCGCGAGA 314
QY 279 AGGAAGTCCGATTCCTGCGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGA 338
DB 315 AGGAAGTCCGATTCCTGCGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGA 374
QY 339 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAACTGATGAGTGGCTGC 398
DB 375 TAAAGACAAAGTCAATCCCTTCACTGAGTGAAGAGAACTGATGAGTGGCTGC 434
QY 399 CCAAAAGGATGACGCGCGGCTTCACTTTTATAGGGCTCAGGTGGCTCCCGGAA 458
DB 435 CCAAAAGGATGACGCGCGGCTTCACTTTTATAGGGCTCAGGTGGCTCCCGGAA 494
QY 459 CATGCTGAGTGGGGGCTCACCCCGGAGTTCATCTGACACCTCCGCAATTTGTAATGA 518
DB 495 CATGCTGAGTGGGGGCTCACCCCGGAGTTCATCTGACACCTCCGCAATTTGTAATGA 554
QY 519 GCCTGTTGGGGTGACAGATAATTTGAGAACAGAAACACATTTGATTTTCATTTCAAC 578

Db 555 |||||
GCCTGTTGGGGTGACAGATTAATTGGAACAGGAAACACATTGAATTTTCATTTCACCC 614
QY 579 AGTTTGCAAAAGCTGAATGAGCCCCCAGTGAGGTCAAGGATTAG 621
615 AGTTTGCAAAAGCTGAATGAGCCCCCAGTGAGGTCAAGGATTAG 657

Search completed: May 28, 2005, 17:32:03
Job time : 521 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 28, 2005, 15:06:20 ; Search time 3078 Seconds
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Title: US-09-869-566-4
Perfect score: 650
Sequence: 1 taattcaccatgtctgcact.....cgactctagagatcccg99 650

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_esc1:*
2: gb_esc2:*
3: gb_hic:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	493.8	76.0	561	1	AI1343258 tb94b05.x
C 2	431.8	66.4	767	1	BG620449 602617582
C 3	408.8	62.9	485	1	AI1014548 0440101.x
C 4	226.2	34.8	372	5	BX283240 BX283240
C 5	225.2	34.6	316	8	AO041691 CIT-HSP-2
C 6	173	26.6	670	7	CF762015 CBS000784
7	108.6	16.7	624	9	CE135149 tigr-gss-
8	52.4	8.1	299	4	BG271067 tigr-gss-
9	52.4	8.1	342	6	BY793571 BY793571
10	52.4	8.1	363	6	BY768696 BY768696
11	52.4	8.1	382	6	BY771752 BY771752
12	52.4	8.1	500	4	BG270250 ib11a12.y
13	52.4	8.1	527	4	BG270248 ib11a09.y
14	52.4	8.1	550	4	BG270253 ib11d08.y
15	52.4	8.1	815	3	AK003082 Mus muscu
16	51.4	7.9	466	7	CF581512 AGENCOURT
17	51.2	7.9	1023	6	BY709409 BY709409
18	51.2	7.9	1219	3	AK009787 Mus muscu
19	51	7.8	498	5	BX282030 BX282030
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21	50.8	7.8	293	2	BB565124 BB565124
22	50.8	7.8	355	2	BB841364 BB841364
23	50.8	7.8	375	5	BY153883 BY153883
24	50.4	7.8	439	4	BG879138 BG879138

25	50.2	7.7	674	7	CF249061 t63e12.y
26	49.4	7.6	302	4	BG880282 BG880282
27	49.4	7.6	386	4	BG880018 t63e11.y
28	49.4	7.6	421	4	BG880821 t63e10.y
29	49.4	7.6	488	4	BG879799 t63e04.y
30	49.4	7.6	498	4	BG271014 t63e05.y
31	49.2	7.6	554	4	BG879105 t63e09.y
32	49.2	7.6	208	4	BG879931 t63e09.y
33	49.2	7.6	273	2	BB562774 BB562774
34	49.2	7.6	421	4	BG879296 t63e03.y
35	49.2	7.6	444	5	BQ126879 t63e10.y
36	49.2	7.6	513	4	BG879198 t63e06.y
37	49.2	7.6	820	7	CF578022 AGENCOURT
38	49.2	7.6	831	7	CF581505 AGENCOURT
39	49.2	7.6	843	7	CF581305 AGENCOURT
40	49.2	7.6	873	7	CF581214 AGENCOURT
41	49.2	7.6	893	7	CF580395 AGENCOURT
42	49.2	7.6	904	7	CF585644 AGENCOURT
43	49.2	7.6	971	7	CF581255 AGENCOURT
44	48.6	7.5	379	5	BX283678 BX283678
45	48.6	7.5	684	7	CF249136 t64e01.y

ALIGNMENTS

RESULT 1
AI1343258/c
LOCUS tb94b05.x1 NCI_CGAP_Col6 Homo sapiens CDNA clone IMAGE:2061969 3',
DEFINITION mRNA sequence.
ACCESSION AI1343258
VERSION AI1343258.1 GI:4080464
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Cloned through the I.M.A.G.E. Consortium/HLN at:
www.bio.lnml.gov/bhrp/image/image.html
Insert Length: 814 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 471.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2061969"
/issue_type="Colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI CGAP Col6"
/note="Organ: colon; Vector: pRTT3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(clones 1057416-1061255, and 1144584-1145351).

ORIGIN Subtraction by Bento Soares and M. Fatima Bonaldo. "

Query Match 76.0%; Score 493.8; DB 1; Length 561;
Best Local Similarity 99.6%; Pred. No. 2.4e-139;
Matches 495; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

130 AACCCGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 189
131 AACCCGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 189
561 AACCCGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 502
190 AATTCATAGCAGATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 249
501 AATTCATAGCAGATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 442
250 TCATCTTGAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 309
441 TCATCTTGAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 382
310 GGGGAGTTTGTCTACTGTGACAGATTAAGGACAAAGTATCATCTCTTCAGCTG 369
381 GGGGAGTTTGTCTACTGTGACAGATTAAGGACAAAGTATCATCTCTTCAGCTG 322
370 AAGAAAGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 429
321 AAGAAAGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 262
430 TTTTATAGGCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 489
261 TTTTATAGGCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 202
490 TTTTATAGGCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 549
201 TTTTATAGGCTCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 142
550 AAGAAAGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 609
141 AAGAAAGAGAAATTCAGATTCATGACGAGATCACAAGTACTGGTCTCGATCTGAG 82
610 GTGAGGATTTAGGCTGAG 626
81 GTGAGGATTTAGGCTGAG 65

RESULT 2
Bg620449 767 bp mRNA linear EST 18-APR-2001
LOCUS 602617582F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4731213 5',
DEFINITION mRNA sequence.
ACCESSION Bg620449
VERSION Bg620449.1 GI:13671820
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 767)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCMI589 row: C column: 22
High quality sequence stop: 709.
Location/Qualifiers
1..767

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4731213"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lib="NIH_MGC_79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggccatcgcc); Site 2: SfiI
(ggccatcgcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 66.4%; Score 431.8; DB 4; Length 767;
Best Local Similarity 94.0%; Pred. No. 2.4e-120;
Matches 482; Conservative 0; Mismatches 27; Indels 4; Gaps 3;

86 CCGGAAATTCAGCTCTTTCAGAGGTCGAAAGTGAAGTGAACCTTAACCCGAAATTC 145
126 CCGCATGAATTTTGTTCACACAGTCCAAAGTGAAGTGAACCTTAACCCGAAATTC 185
146 GATTCATGACAGATTCACAAAGTACGTCCTGACCTGCGGAATTCATAGAGCTTC 205
186 GATTCATGACAGATTCACAAAGTACGTCCTGACCTGCGGAATTCATAGAGCTTC 245
206 CAGATTAACATACATACGCGCAGAGATCTTTCATATGATTCATCTTTCAGCTGAG 265
246 CAGATTAACATACATACGCGCAGAGATCTTTCATATGATTCATCTTTCAGCTGAG 305
266 CCTTCGCGAGAAAGAAATTCGATTCCTTTCGAGGCTCTTAAGGAGGATTTGTCTCT 325
306 CCTTCGCGAGAAAGAAATTCGATTCCTTTCGAGGCTCTTAAGGAGGATTTGTCTCT 364
326 ACTTGACAGAGATTAAGGACAAAGTACATCCCTTCAGCTGAGGAGGAGAAATTCGA 385
365 ACTTGACAGAGATTAAGGACAAAGTACATCCCTTCAGCTGAGGAGGAGAAATTCGA 424
386 TGAAGCTGCTGCCCAAAAGAAATTCAGACGCGGCTTCATCTTTATAGGCTCAGG 445
425 TGAAGCTGCTGCCCAAAAGAAATTCAGACGCGGCTTCATCTTTATAGGCTCAGG 484
446 -TGGGCTCTGGAACATGCTGAGTCTGAGGCTCAGCCCGGATGTTTATCTGACCTTC 504
485 TTGGGCTCTGGAACATGCTGAGTCTGAGGCTCAGCCCGGATGTTTATCTGACCTTC 544
505 TGCATTTGATGAGCTGTTGGGCTGACAGTAAATTT--GAGAAACAGAAACATCTG 562
545 TGCATTTGATGAGCTGTTGGGCTGACAGTAAATTTGAGAAACAGGAAACATCTG 604
563 AATTTTCATTTGACAGTTTGCAGGAGTGA 595
605 ACTTTTCATTTGACAGTTTGCAGGAGTGA 637

RESULT 3
A1014548/c 485 bp mRNA linear EST 27-AUG-1998
LOCUS A1014548
DEFINITION ou40f01.x1 Soares_NFI_T.GBC_S1 Homo sapiens cDNA clone
IMAGE:1628761 3', mRNA sequence.
ACCESSION A1014548
VERSION A1014548.1 GI:3228929
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 485)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert length: 1052 Std Error: 0.00
 Seq primer: -40m3 fwd. ET from Amersham
 High quality sequence stop: 424.

FEATURES

source

1..485
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1628761"
 /lab_host="DH10B"
 /note="Organs: Soares NFL T GBC S1"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung, NBHL19W, testis NHT, and B-cell
 NCI CGAP GCBI) were mixed, and 88 circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1 M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 62.9%; Score 408.8; DB 1; Length 485;
Best Local Similarity 99.5%; Pred. No. 2.2e-113;
Matches 410; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

215 ACTACATAGCCGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCGCGG 274
 485 ACTACATAGCCGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCGCGG 426
 275 AGAAGAAGAGTCGATCTCTGCGGGTCTTAAAGGAGTTTGTCTTACTGTACA 334
 425 AGAAGAAGAGTCGATCTCTGCGGGTCTTAAAGGAGTTTGTCTTACTGTACA 366
 335 AGATTAAGACAAATCATTCATCCCTTCAAGCTGAAGAGAAAGTGAAGCTGG 394
 365 AGATTAAGACAAATCATTCATCCCTTCAAGCTGAAGAGAAAGTGAAGCTGG 306
 395 CTGCCCAAAAGAAATAGACGCGGCGCTTCACTTTTATAGGGCTCAAGTGGCTCT 454
 305 CTGCCCAAAAGAAATAGACGCGGCGCTTCACTTTTATAGGGCTCAAGTGGCTCT 246
 455 GGAACATGCTGAGTGGCGGCTCAACCCGAGATGTTCATCTGCACTCTGCAATTGA 514
 245 GGAACATGCTGAGTGGCGGCTCAACCCGAGATGTTCATCTGCACTCTGCAATTGA 186
 515 ATGAGCTGTGGGTGACAGATTAATTTGAAGACGAAACACATTTGAATTTTCATTTC 574
 185 ATGAGCTGTGGGTGACAGATTAATTTGAAGACGAAACACATTTGAATTTTCATTTC 126
 575 AACCAAGTTTGAAGAGTGAAGAGCCGAGAGAGTCAAGCATTTAGGGTAC 626
 125 AACCAAGTTTGAAGAGTGAAGAGCCGAGAGAGTCAAGCATTTAGGGTAC 74

RESULT 4
LOCUS BX283240 372 bp mRNA linear EST 04-MAR-2003
DEFINITION BX283240 NIH_MGC_79 Homo sapiens cDNA clone IMAGE958C221589;
IMAGE: 4731213, mRNA sequence.
ACCESSION BX283240
VERSION BX283240.1 GI:28847694

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 372)
 Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Radloff, U., Schneider, D., and Korn, B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGE958C221589.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No. 972)
<http://www.rzpd.de/CloneCards/cgl-bin/showLib.pl.cgi/response?libNo=972> Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

This clone is available royalty-free from RZPD;
 contact RZPD (clone@rzpd.de) for further information. Seq primer:
 PCW-M13u, Primer sequence: CGTTGTAACGACGGCCAGT.

FEATURES
 source
 Location/Qualifiers

1..372
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE958C221589 ; IMAGE:4731213"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH_MGC_79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggccgctcgcc); Site 2: SfiI
 (ggccatcagcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGGCCATTTAGGCC-3'
 and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGGCGGCGGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 34.8%; Score 226.2; DB 5; Length 372;
Best Local Similarity 94.7%; Pred. No. 1.4e-57;
Matches 234; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

86 CCGGAATTCAGCTCTTTCAGAGGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTC 145
 126 CCGCATGAATTTTGTTCACAAAGTCCAAAGTGAAGAACTTAAACCGAAGAAATTC 185
 146 GCATTCATGACCAAGATGACAAAGTACGTGCTGAGCTCGGGAGTCAATGAGATTC 205
 186 GCATTCATGACCAAGATGACAAAGTACGTGCTGAGCTCGGGAGTCAATGAGATTC 245
 206 CAGATTAACAACTACATAGCCGAGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCAG 265
 246 CAGATTAACAACTACATAGCCGAGAGATCTTCTTGACATTAAGCTCATCTTGAAGCTCAG 305
 266 CCTTGGCGGAGAAAGAGTCCGATTTCTCTGGGGGTCTCTTAAAGGAGATTTGTCTCT 325
 306 CCTTGGCGGAGAAAGAGTCCGATTTCTCTGGGGGTCTCTTAAAGGAGATTTGTCTCT 365
 326 ACTGTGA 332
 366 ACTGTGA 372

RESULT 5

A0041691/c 316 bp DNA linear GSS 14-JUL-1998
LOCUS A0041691
DEFINITION CIT-HSP-2326018.TR CIT-HSP Homo sapiens genomic clone 2326018,
genomic survey sequence.
ACCESSION A0041691
VERSION A0041691.1 GI:3310962
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 316)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
TITLE Unpublished (1998)
JOURNAL Other GSSs: CIT-HSP-2326018.TV
COMMENT Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
1. 316
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2326018"
/sex="Male"
/cell_type="Sperm"
/note="lib="CIT-HSP"
/vector="pBelobAC11, Site_1: HindIII, Site_2:
HindIII"
ORIGIN
Query Match 34.6%; Score 225.2; DB 8; Length 316;
Best Local Similarity 98.7%; Pred. No. 2.7e-57;
Matches 227; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY GCCCAAGGAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGG 456
DB GCCCAAGGAATCAGACGCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGG 257
QY AACATCTGAGTCGAGCGGCTCAACCGGATGTTATATGAGGCTCAGGTGGGCTCTGG 516
DB AACATCTGAGTCGAGCGGCTCAACCGGATGTTATATGAGGCTCAGGTGGGCTCTGG 197
QY GAGCGTGGGGGTGACAGTAATTTGAGAACAGAAACACATTGAATTTTCATTCAA 576
DB GAGCGTGGGGGTGACAGTAATTTGAGAACAGAAACACATTGAATTTTCATTCAA 137
QY CCAGTTTGCAAAAGCTGAATGAGCCCGAGTGAGGTGAGGATTAGGATAC 626
DB CCAGTTTGCAAAAGCTGAATGAGCCCGAGTGAGGTGAGGATTAGGATAC 87
RESULT 6
CF762015 670 bp mRNA linear EST 17-OCT-2003
LOCUS CF762015
DEFINITION CCL000784 Bos taurus skin cDNA library Bos taurus cDNA clone
ACCESSION CF762015
VERSION CF762015.1 GI:37711233
KEYWORDS EST.

SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 670)
Wang,Y.H., McWilliam,S. and Lehnert,S.
Transcription profiling of cattle skin
Unpublished (2003)
JOURNAL Contact: Dr Yonghong Wang
Functional Genomics lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonghong.Wang@csiro.au
Plate: 18 row: D column: 12.
FEATURES
source
1. 670
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL000784"
/sex="female"
/tissue_type="pooled"
/dev_stage="Adult"
/lab_host="X11-BluemRF'strain"
/clone_lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site_1: EcoRI;
Site_2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."
ORIGIN
Query Match 26.6%; Score 173; DB 7; Length 670;
Best Local Similarity 62.4%; Pred. No. 3.3e-41;
Matches 305; Conservative 0; Mismatches 180; Indels 4; Gaps 2;
QY AAGTCCAAAGGAAGGAATTAACCCGAAAGAAATTCAGCATTCAGACAGATCAGAA 167
DB AAGTCCAAAGGAAGGAATTAACCCGAAAGAAATTCAGCATTCAGACAGATCAGAA 243
QY AGTACTGTCCTGAGACTCGGAGATCTCATAGCAGTTCAGATTAACCTACATGCGCC 227
DB AGTACTGTCCTGAGACTCGGAGATCTCATAGCAGTTCAGATTAACCTACATGCGCC 303
QY TATTTTGGTCTGAGCTCAGTACCTGAGACAGTTCAGATTAAGATTAAGATTAAGTCC 287
DB TATTTTGGTCTGAGCTCAGTACCTGAGACAGTTCAGATTAAGATTAAGATTAAGTCC 363
QY AACTACCTACTTATATATATATCTCCGAGTGAAGTCAAGTATGAGAACTAATGATACCC 347
DB AACTACCTACTTATATATATATCTCCGAGTGAAGTCAAGTATGAGAACTAATGATACCC 423
QY GATTCCTCGGGGGTCTCAAGAGGGAGTCTTCTCACTGACAGATTAAGAGACA 407
DB GATTCCTCGGGGGTCTCAAGAGGGAGTCTTCTCACTGACAGATTAAGAGACA 480
QY AAGTCATCCATCCCTTCAGCTGAGAGAGAGAGAACTGATGAAGCTGAGTCCCAAGGA 467
DB AAGTCATCCATCCCTTCAGCTGAGAGAGAGAGAACTGATGAAGCTGAGTCCCAAGGA 540
QY CA---AGCATCCCTGAGAGCTGAAGACTAAGAACTTCACAACTGAGTCCCAAGGA 527
DB CA---AGCATCCCTGAGAGCTGAAGACTAAGAACTTCACAACTGAGTCCCAAGGA 600
QY ATCAGACGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGGA 467
DB ATCAGACGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGGA 540
QY GTGCGGGGCTCACCCCGATGTTGATCTGACCTCCGCAATGTAATGAGCTGTTGG 527
DB GTGCGGGGCTCACCCCGATGTTGATCTGACCTCCGCAATGTAATGAGCTGTTGG 600
QY GTGAGCTGCCATCTCAATAGATCTCTGACCTTCCCAATCCTGGCAACAGTCTT 587
DB GTGAGCTGCCATCTCAATAGATCTCTGACCTTCCCAATCCTGGCAACAGTCTT 659
QY GGTGACAGATTAATTTGAGAACAGAAACACATTGAATTTTCATTCAA 587
DB GGTGACAGATTAATTTGAGAACAGAAACACATTGAATTTTCATTCAA 659
QY ATTG---CAAGAGCTCAGAGTGAAGAGAAACACACTGAGTTTCAATTCGGCGCATTA 596
DB ATTG---CAAGAGCTCAGAGTGAAGAGAAACACACTGAGTTTCAATTCGGCGCATTA 596

Db 660 AGCTGAAT 668

RESULT 7
CE135149

LOCUS CE135149 624 bp DNA linear GSS 25-SEP-2003

DEFINITION tigr-gss-dog-17000326525085 Dog Library Canis familiaris genomic,

ACCESSION CE135149

VERSION CE135149.1 GI:35239139

KEYWORDS GSS.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 624)

AUTHORS Kirchner, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Ruch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis

JOURNAL Science 301 (5641), 1898-1903 (2003)

MEDLINE 22875432

PUBMED 14512627

COMMENT Contact: Kirchner EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirchner@tigr.org
Classes: shotgun.

FEATURES
source Location/Qualifiers
1..624
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN

Query Match 16.7%; Score 108.6; DB 9; Length 624;
Best Local Similarity 83.7%; Pred. No. 1.6e-21;
Matches 123; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 226 CCAGAGATCTTTGATTAAGCTTCATCTTGAGCTCAGCTTCGCGAGAAAGGAAGT 285

Db 247 CCAGAGATCTTTGATTAAGCTTCATCTTGAGCTCAGCTTCGCGAGAAAGGAAGT 306

QY 286 CGATTTCTCTGGGGGCTCTTAAGGGAGTTTGTCTCTAATGTGACAAAGATAAGGA 345

Db 307 CCAATTCCTTTGGCAGTCTGAAGAGAGCTTTGTCTCTGTGTGAAGAGACAGAGA 366

QY 346 CAAAGTCATCATCCCTTCAGCTGAAG 372

Db 367 CAAAGCCATCATCTTCAGCTGAAG 393

RESULT 8
BG271067

LOCUS BG271067 299 bp mRNA linear EST 13-MAR-2002

DEFINITION IBOH11.Y1 Melton Mouse Adult Pancreas 1 Mus musculus cDNA clone

ACCESSION BG271067

VERSION BG271067.1 GI:12978839

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 299)

AUTHORS Melton, D., Meadows, A., Clifton, S., Hallier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blistein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T., Jackson, Y. and Bowers, Y.

TITLE WashU-Harvard Pancreas EST Project

JOURNAL Unpublished (2000)

COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)

MGI:1851677 This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov

Seq primer: -40RP from Gibco

High quality sequence stop: 292.

FEATURES
source Location/Qualifiers
1..299
/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5646957"
/sex="Male"
/tissue_type="Total Pancreas"
/dev_stage="Adult"
/lab_host="TOP10"
/clone_lib="Melton Mouse Adult Pancreas 1"
/note="Organ: Pancreas; Vector: pZeo-2; Site 1: Not I; Site 2: Xho I; Library constructed using SuperScript plasmid library kit (Life Technologies). cDNA made by oligo-dT priming. Xho I site destroyed during cloning. Size-selected by column fractionation. Primary library, unamplified."

ORIGIN

Query Match 8.1%; Score 52.4; DB 4; Length 299;
Best Local Similarity 79.5%; Pred. No. 0.00019;
Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 5 TCACATGTCGACATTCATCTAGCTCTTGTGAGAGCTCAGTGTGACTACAAAG 64

Db 23 TCACATGATGACATCTTCATCTAGCTTCAGCTTCGAGAGCTCTGTGCTTCCTG 82

QY 65 ACATGACGACAAAGCTTG 82

Db 83 ATGATGATGACAAAGATTG 100

RESULT 9
BY793571

LOCUS BY793571 342 bp mRNA linear EST 23-MAR-2004

DEFINITION BY793571 RIKEN full-length enriched, 17.5 days embryo whole body

ACCESSION BY793571

VERSION BY793571.1 GI:39720210

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 342)

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Carninci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M., Aizawa, K., Arikawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Otsu, N., Fukuda, S., Sato, K., Watabiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A.,

TITLE
Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Paven, W., Aidinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mommaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
Targeting a complex transcritpome: the construction of the mouse full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)

JOURNAL
MEDLINE
PUBMED
22703353
12819125

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

FEATURES
source
Location/Qualifiers
1..342
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="L930285A07"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_1ib="RIKEN full-length enriched, 17.5 days embryo whole body"

ORIGIN
Query Match
Best Local Similarity 8.1%; Score 52.4; DB 6; Length 342;
Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY
5 TCACCATGTCGACCTTGATCTAGCTCTGTTGGAGCTGCAGTGTGCTGACACAAAG 64
|||||
11 TCACCATGATGACATCTTGATCTAGCCCTTGTGGAGCTGCTGTGCTTCCCTGTGG 70
|||||

Db
65 ACGATGACGACAAAGCTTG 82
|||||
71 ATGATGATGACAAAGATTG 88
|||||

QY
65 ACGATGACGACAAAGCTTG 82
|||||

Db
71 ATGATGATGACAAAGATTG 88
|||||

RESULT 10
BY768696 363 bp mRNA linear EST 22-MAR-2004
BY768696 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930023M20 5', mRNA sequence.
BY768696 BY768696.1 GI:39693687
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 363)
Carninci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Paven, W., Aidinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mommaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.

REFERENCE
AUTHORS

TITLE
Targeting a complex transcritpome: the construction of the mouse full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)

JOURNAL
MEDLINE
PUBMED
22703353
12819125

COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

FEATURES
source
Location/Qualifiers
1..363
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="L930023M20"
/tissue_type="whole body"
/dev_stage="17.5 days embryo"
/clone_1ib="RIKEN full-length enriched, 17.5 days embryo whole body"

ORIGIN
Query Match
Best Local Similarity 8.1%; Score 52.4; DB 6; Length 363;
Matches 62; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY
5 TCACCATGTCGACCTTGATCTAGCTCTGTTGGAGCTGCAGTGTGCTGACACAAAG 64
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11 TCACCATGATGACATCTTGATCTAGCCCTTGTGGAGCTGCTGTGCTTCCCTGTGG 70
|||||

Db
65 ACGATGACGACAAAGCTTG 82
|||||
71 ATGATGATGACAAAGATTG 88
|||||

QY
65 ACGATGACGACAAAGCTTG 82
|||||

Db
71 ATGATGATGACAAAGATTG 88
|||||

RESULT 11
BY771752 382 bp mRNA linear EST 23-MAR-2004
BY771752 RIKEN full-length enriched, 17.5 days embryo whole body
Mus musculus cDNA clone L930056N12 5', mRNA sequence.
BY771752 BY771752.1 GI:39698390
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 382)
Carninci, P., Waki, K., Shiraki, T., Kono, H., Shibata, K., Itoh, M., Aizawa, K., Arakawa, T., Ishii, Y., Sasaki, D., Bono, H., Kondo, S., Sugahara, Y., Saito, R., Osato, N., Fukuda, S., Sato, K., Watahiki, A., Hirozane-Kishikawa, T., Nakamura, M., Shibata, Y., Yasunishi, A., Kikuchi, N., Yoshiki, A., Kusakabe, M., Gustincich, S., Beisel, K., Paven, W., Aidinis, V., Nakagawara, A., Held, W. A., Iwata, H., Kono, T., Nakachi, H., Lyons, P., Wells, C., Hume, D. A., Fagiolini, M., Hensch, T. K., Brinkmeier, M., Camper, S., Hirota, J., Mommaerts, P., Muramatsu, M., Okazaki, Y., Kawai, J. and Hayashizaki, Y.
Targeting a complex transcritpome: the construction of the mouse full-length cDNA encyclopedia
Genome Res. 13 (6B), 1273-1289 (2003)

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MEDLINE
PUBMED
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12819125


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ORIGIN
Query Match      8.1%; Score 52.4; DB 3; Length 815;
Best Local Similarity 79.5%; Pred. No. 0.00027;
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QY      5 TCACCAATGCTGCACCTTCTGATCCTAGCTCTTGTGTGAGCTGCAGTTGCTGACTACAAAG 64
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QY      65 ACGATGACGACAAGCTTG 82
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